

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 27, 2006, 17:55:43 ; Search time 187 Seconds
(without alignments)
472.273 Million cell updates/sec

Title: US-10-696-259-6
Perfect score: 1067
Sequence: 1 MAWMLLLILIMVHPGSCALW.....APLPPPCGSSAHLPPVPG 201

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21.*
1: Geneseqp1980s.*
2: Geneseqp1990s.*
3: Geneseqp2000s.*
4: Geneseqp2001s.*
5: Geneseqp2002s.*
6: Geneseqp2003as.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*
9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1067	100.0	201	2	RAY06403	Asy06403 Human B-c
2	1067	100.0	201	9	ADY16489	Ady16489 PRO polyp
3	1067	100.0	201	9	AEA40207	Aea40207 Human nat
4	876	82.1	190	4	RAE02769	Aae02769 Human Nkp
5	876	82.1	190	8	ADO19810	Ado19810 Human PRO
6	876	82.1	190	8	ADQ30923	Adq30923 Human Nkp
7	874	81.9	190	2	RAY06401	Asy06401 Human B-c
8	859	80.5	177	2	RAY06402	Asy06402 Human B-c
9	859	80.5	177	9	ADY16598	Ady16598 PRO polyp
10	713	66.8	135	5	RAE13109	Aae13109 Human Nkp
11	713	66.8	369	5	RAE19110	Aae19110 Human Nkp
12	632	59.2	120	4	RAE02771	Aae02771 Human Nkp
13	632	59.2	120	8	ADQ30924	Adq30924 Human Nkp
14	608.5	57.0	382	8	ADP48750	Adp48750 Human Nkp
15	608.5	57.0	382	9	AEA40208	Aea40208 Human CD5
16	143	13.4	28	9	AEA40197	Aea40197 Peptide (
17	125.5	11.8	246	5	AAE20273	Aae20273 Human lun
18	125	11.7	212	2	AAE60134	Aae60134 CTLA4 rec
19	125	11.7	212	2	AAE77642	Aae77642 Full leng
20	125	11.7	212	2	AAE43479	Aae43479 Amino aci
21	125	11.7	212	2	AAW81584	Aaw81584 Human CTL
22	125	11.7	212	5	ABB78106	Abb78106 Amino aci
23	125	11.7	212	5	AAU75124	Aau75124 Human CTL
24	125	11.7	212	5	AAU75132	Aau75132 Human CTL

25	125	11.7	212	6	ABP56715	Abp56715 Human CTL
26	125	11.7	212	7	ADD89013	Add89013 CTLA4 rec
27	125	11.7	212	8	ADQ89550	Adq89550 CTLA4 rec
28	125	11.7	212	9	ADP95980	Adp95980 Human CTL
29	125	11.7	212	8	ADW98655	Adw98655 Human CTL
30	125	11.7	212	9	ADX08914	Adx08914 Protein s
31	123	11.5	212	5	AAU75126	Aau75126 Human CTL
32	122.5	11.5	211	2	AAW87560	Aaw87560 Human CTL
33	122	11.4	212	5	AAU75127	Aau75127 Human CTL
34	122	11.4	212	5	AAU75131	Aau75131 Human CTL
35	122	11.4	212	5	AAU75130	Aau75130 Human CTL
36	121.5	11.4	232	6	ABU08020	Abu08020 Monoclonal
37	121.5	11.4	232	7	ADF65784	Adf65784 Human ant
38	121.5	11.4	232	8	ADJ92520	Adj92520 Human SOJ
39	121	11.3	212	5	AAU75133	Aau75133 Human CTL
40	118.5	11.1	139	5	AAU75565	Aau75565 Murine T
41	118.5	11.1	223	3	AAU75129	Aau75129 Human CTL
42	118.5	11.1	223	5	AAU74509	Aau74509 Human cyt
43	118.5	11.1	223	5	AAU74508	Aau74508 Human cyt
44	118.5	11.1	223	8	ADP12469	Adp12469 Protein e
45	118.5	11.1	223	8	ADP55366	Adp55366 Human PRO

ALIGNMENTS

RESULT 1
ID AAY06403 standard; protein; 201 AA.
XX AAY06403;
XX
XX 20-SEP-1999 (first entry)
XX Human B-cell myelin oligodendrocyte glycoprotein BMOG.
XX
XX MBOG; B-cell myelin oligodendrocyte glycoprotein; human;
XX signal transduction; immunomodulator; antiinflammatory;
XX autoimmune disease; inflammation; gene therapy; diagnosis.
XX
XX Homo sapiens.
XX
XX
XX Key Location/Qualifiers
FT Peptide 1..12
FT Protein /note= "leader peptide"
FT Protein 13..201
FT Protein /note= "mature protein"
FT Modified-site 42
FT Modified-site /note= "N-glycosylated"
FT Modified-site 68
FT Modified-site /note= "N-glycosylated"
FT Modified-site 121
FT Domain /note= "N-glycosylated"
FT Peptide 139..162
FT Peptide /note= "transmembrane domain"
FT Peptide 166..201
FT Peptide /note= "alternatively spliced C-terminal end"
XX WO9923867-A2.
XX
XX 20-MAY-1999.
XX
XX 05-NOV-1998; 98WO-US023826.
XX
XX 07-NOV-1997; 97US-0064761P.
XX (BIOJ) BIOGEN INC.
XX
XX Browning J;
XX
XX WPI; 1999-418423/35.
XX N-PSDB; AAX59349.
XX

BEST AVAILABLE COPY

PT Novel B-cell myelin oligodendrocyte glycoproteins.

XX Claim 2; Page 43; 43pp; English.

XX This sequence represents human BMOG, a novel member of the B cell myelin
CC oligodendrocyte glycoprotein family that is expressed by germinal centre
CC B cells. 3 C-terminal splice variants (see AAY06401-03) of BMOG were
CC identified. The protein is present primarily in the spleen, in lymph
CC nodes and in germinal centre B cells. It may have immunoregulatory
CC functions, and soluble or chimeric fusion proteins of BMOG may be used to
CC regulate the immune system in autoimmune or inflammatory disease. Vectors
CC comprising BMOG, prokaryotic and eukaryotic host cells, and a method of
CC producing BMOG using these transformed host cells are also provided. BMOG
CC polypeptides can be used for modulating the immune system of a subject or
CC to inhibit signal transduction in a cell expressing BMOG by contacting it
CC with a soluble BMOG protein. The nucleic acid can be used for gene
CC therapy. The protein can also be used to target a toxin, imaging agent or
CC radionuclide to a cell expressing BMOG. (All claimed)

XX Sequence 201 AA;

Query Match 100.0%; Score 1067; DB 2; Length 201;

Best Local Similarity 100.0%; Pred. No. 4.2e-93;

Matches 201; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAMLLILIMVHPGSCALWVSQPPPIRTLEGSSAFPCSFNASQGRLAIGSVTWERDEV 60

Db 1 MAMLLILIMVHPGSCALWVSQPPPIRTLEGSSAFPCSFNASQGRLAIGSVTWERDEV 60

Qy 61 VPGKEVRNGTPEFRGRPLASSRFLHDHQAELHIRDVRGHDASIYVCRVEVLGLGVGTG 120

Db 61 VPGKEVRNGTPEFRGRPLASSRFLHDHQAELHIRDVRGHDASIYVCRVEVLGLGVGTG 120

Qy 121 NGTRLVVEKEHPQLGAGTVLLIRAGFYAVSFLSVAVGSTVYQKCLTWKGRPRQLPAVV 180

Db 121 NGTRLVVEKEHPQLGAGTVLLIRAGFYAVSFLSVAVGSTVYQKCLTWKGRPRQLPAVV 180

Qy 181 PAPLPPPCGSSAHLPPVPGG 201

Db 181 PAPLPPPCGSSAHLPPVPGG 201

ADY16489

ADY16489 standard; protein; 201 AA.

AC ADY16489;

DE 05-MAY-2005 (first entry)

XX PRO polypeptide SEQ ID NO 2295.

XX Antinflammatory; Immune disorder; Dermatological; Immunosuppressive;

XX Antirheumatic; Antiarthritic; Osteopathic; Hemostatic; Antianemic;

XX Antithyroid; Antidiabetic; Nephrotropic; CNS-Gen.; Hepatotropic;

XX Virucide; Gastrointestinal-Gen.; Antipsoriatic; Antiasthmatic;

XX Antiallergic; ds; gene; diagnosis.

XX Homo sapiens.

XX WO2005016962-A2.

XX 24-FEB-2005.

XX 11-AUG-2004; 2004WO-US026249.

XX 11-AUG-2003; 2003US-0493546P.

XX (GETH) GENENTECH INC.

XX Abbas A, Clark H, Ouyang W, Williams MP, Wood WI, Wu TD;

XX WPI; 2005-182330/19.

XX New nucleic acid encoding PRO polypeptide, useful for diagnosing and
PT treating an immune related disorder, e.g. systemic lupus erythematosus,
PT rheumatoid arthritis, osteoarthritis, thyroiditis, or diabetes mellitus.
XX Claim 8; SEQ ID NO 2295; 158pp; English.

XX The invention relates to an isolated nucleic acid encoding a PRO
CC polypeptide. The polypeptide, agonist or an antagonist, antibody,
CC composition, and method are useful for diagnosing and treating an immune
CC related disorder, e.g. systemic lupus erythematosus, rheumatoid
CC arthritis. The present sequence represents a DNA encoding a PRO
CC polypeptide.

XX Sequence 201 AA;

Query Match 100.0%; Score 1067; DB 9; Length 201;

Best Local Similarity 100.0%; Pred. No. 4.2e-93;

Matches 201; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAMLLILIMVHPGSCALWVSQPPPIRTLEGSSAFPCSFNASQGRLAIGSVTWERDEV 60

Db 1 MAMLLILIMVHPGSCALWVSQPPPIRTLEGSSAFPCSFNASQGRLAIGSVTWERDEV 60

Qy 61 VPGKEVRNGTPEFRGRPLASSRFLHDHQAELHIRDVRGHDASIYVCRVEVLGLGVGTG 120

Db 61 VPGKEVRNGTPEFRGRPLASSRFLHDHQAELHIRDVRGHDASIYVCRVEVLGLGVGTG 120

Qy 121 NGTRLVVEKEHPQLGAGTVLLIRAGFYAVSFLSVAVGSTVYQKCLTWKGRPRQLPAVV 180

Db 121 NGTRLVVEKEHPQLGAGTVLLIRAGFYAVSFLSVAVGSTVYQKCLTWKGRPRQLPAVV 180

Qy 181 PAPLPPPCGSSAHLPPVPGG 201

Db 181 PAPLPPPCGSSAHLPPVPGG 201

RESULT 3

AEA40207

ID AEA40207 standard; protein; 201 AA.

AC AEA40207;

XX 11-AUG-2005 (first entry)

XX Human natural cytotoxicity receptor, NKp30.

XX natural cytotoxicity receptor; natural killer cell; lymphocyte; membrane;

XX tumor; cell disintegration; antibody; NKp30; hyperproliferation;

XX cytostatic; receptor.

XX Homo sapiens.

XX WO2005051973-A2.

XX 09-JUN-2005.

XX 24-NOV-2004; 2004WO-IL001081.

XX 25-NOV-2003; 2003US-0524648P.

XX (YISS) YISSUS RES & DEV CO.

XX (UYNE) UNIV BEN-GURION NEGEV RES & DEV.

XX Mandelboim O, Porgador A;

XX WPI; 2005-405348/41.

XX New peptides derived from specific natural cytotoxicity receptors and

XX capable of binding to membrane-associated biomolecules of tumor cells,

XX useful for targeting tumor cells to diagnose or treat benign and/or

XX malignant tumors.

PS Disclosure; SEQ ID NO 13; 86pp; English.

XX The invention relates to isolated peptide fragments of a natural
CC cytotoxicity receptor (NCR) of natural killer (NK) cells, or active
CC fragments, analogs or derivatives, wherein the peptide fragment is
CC capable of binding to a membrane-associated biomolecule of a tumor cell,
CC and the biomolecule comprises at least one sulfated polysaccharide, and
CC serves as the binding site of the NCR mediating the lysis of tumor cells
CC by NK cells, with the proviso that the peptide is other than a full
CC length NCR polypeptide or an isolated NCR extracellular domain. Also
CC described are: (1) an antibody that recognizes an epitope on a target
CC membrane-associated biomolecule of a tumor cell, the biomolecule
CC comprising at least one sulfated polysaccharide and mediating the lysis
CC of tumor cells by NK cells via the NCR; (2) a method of targeting a tumor
CC cell in a subject via an NCR-dependent mechanism; and (3) a method of
CC identifying peptides derived from NCR which are capable of binding to a
CC membrane-associated sulfated polysaccharide of a tumor cell. The peptide
CC fragment comprises 7-120, 8-100 or less than about 50 contiguous amino
CC acids. The peptide is a fragment of NCR selected from Nkp44, Nkp30 and
CC Nkp46. It is a fragment of the D2 domain of Nkp46 comprising a sequence
CC fully defined in the specification (SEQ ID NOS: 1 and 2), or a fragment
CC of Nkp30 selected from a sequence fully defined in the specification (SEQ
CC ID NOS: 3 and 4). Alternatively, the peptide is a fragment of Nkp44
CC having a sequence fully defined in the specification (SEQ ID NO: 5). The
CC membrane-associated biomolecule is selected from a glycosaminoglycan and
CC a proteoglycan. The antibody is capable of blocking the binding of NK
CC cells via NCR to membrane-associated sulfated polysaccharide biomolecules
CC in a cell, therefore, inhibiting NCR-dependent cell lysis associated with
CC autoimmunity. The peptides and antibodies of the invention are useful for
CC targeting a tumor cell in a subject via an NCR-dependent mechanism. The
CC composition and methods of the invention are useful for targeting tumor
CC cells to diagnose and/or treat benign and malignant tumors or
CC proliferative diseases. This sequence represents human natural
CC cytotoxicity receptor, Nkp30.

XX
SQ Sequence 201 AA;

Query Match 100.0%; Score 1067; DB 9; Length 201;
Best Local Similarity 100.0%; Pred. No. 4.2e-93;
Matches 201; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAWMLLLILIMVHPGSCALWVSQPPEIRTLGSSAFILPCSFNASQGRLAIGSVTWFDE 60
Db 1 MAWMLLLILIMVHPGSCALWVSQPPEIRTLGSSAFILPCSFNASQGRLAIGSVTWFDE 60
Qy 61 VPGKEVRNGTPEFGRRLAPLASSRFLDHQAEHLIRDVGRGHDSIYVCRVEVLGLGVGTG 120
Db 61 VPGKEVRNGTPEFGRRLAPLASSRFLDHQAEHLIRDVGRGHDSIYVCRVEVLGLGVGTG 120
Qy 121 NGTRLVVEKEHPQLGAGTVLLLRAGFYAVSFLSVAVGSTVYVQKCLTWKGRQLPAVV 180
Db 121 NGTRLVVEKEHPQLGAGTVLLLRAGFYAVSFLSVAVGSTVYVQKCLTWKGRQLPAVV 180
Qy 181 PAPLPFPGGSAHLLPPVPGG 201
Db 181 PAPLPFPGGSAHLLPPVPGG 201

RESULT 4

AAE02769

ID AAE02769 standard; protein; 190 AA.

XX

AC AAE02769;

XX

DT 06-AUG-2001 (first entry)

XX Human Nkp30 receptor.

DE Human, Nkp30 receptor; natural killer cell; cytostatic; antimicrobial;

XX melanoma; hepatocarcinoma; lung adenocarcinoma; viral infection; tumour;

KW immunosuppressant; antiviral; drug; grafting enhancement; leukaemia;

KW therapy.

XX

OS Homo sapiens.

XX Key Location/Qualifiers

PH Peptide 1..18 /label= Signal_peptide

FT Protein 19..190 /label= Mature_Nkp30_receptor_protein

FT Region 19..138 /label= Extracellular_region

FT /note= "Forms an immunoglobulin (Ig) V-like domain"

FT Modified-site 42 /note= "N-glycosylation site"

FT Modified-site 121 /note= "N-glycosylation site"

FT Region 139..157 /label= Transmembrane_region

FT Region 158..190 /label= Intracellular_region

XX WO200136630-A2.

XX 25-MAY-2001.

XX 15-NOV-2000; 2000WO-EP011697.

XX 15-NOV-1999; 99CA-02288307.

XX 15-NOV-1999; 99US-00440514.

XX (INNA-) INNATE PHARMA SAS.

XX (UYGE-) UNIV GENOVA.

XX Moretta A, Bottino C, Biassoni R;

XX WPI; 2001-329221/34.

XX N-PSDB; AAD06564.

XX Novel compound, useful for detection and/or quantifying the presence of
FT NK cells, comprises the amino acid sequences of the Nkp30 molecule.

XX Claim 1; Fig 7B; 83pp; English.

XX The invention relates to human Nkp30 receptor and its corresponding cDNA
CC molecule which is involved in natural cytotoxicity mediated by natural
CC killer (NK) cells and antibodies that identify the same. Nkp30 receptor
CC is a member of immunoglobulin super family (Ig-SF). Nkp30 is selectively
CC expressed on the surface of human mature NK cells. Nkp30 and its cDNA are
CC useful for detecting and/or quantifying the presence of NK cells in a
CC biological sample. The invention also provide kits for detecting and/or
CC quantifying the presence of NK cells, for the selective removal of NK
CC cells from a biological sample, for the positive and selective
CC purification of NK cells from a biological sample and for the in vitro
CC stimulation of NK cell cytotoxicity. The invention further provides a
CC pharmaceutical composition which is used as a drug for grafting
CC enhancement, graft versus host (GvH) inhibition, stimulation of graft
CC versus tumour (GvT) and especially graft versus leukaemia (GvL), and for
CC the prevention, palliation and/or therapy of solid or liquid tumours,
CC such as melanoma, hepatocarcinoma and lung adenocarcinoma, and/or
CC microorganism, notably viral infection. Nkp30 antibodies are useful for
CC identifying Nkp30 natural ligands and allow assessment of the level of
CC surface Nkp30 ligand expressed on an NK-susceptible target cell and the
CC comparison of this level to the standard physiological one. Hence Nkp30
CC antibodies are useful in the diagnosis of tumours or of infection. The
CC present sequence is human Nkp30 receptor

XX
SQ Sequence 190 AA;

Query Match 82.1%; Score 876; DB 4; Length 190;

Best Local Similarity 89.2%; Pred. No. 5.9e-75;

Matches 173; Conservative 2; Mismatches 7; Indels 12; Gaps 2;

Qy 1 MAWMLLLILIMVHPGSCALWVSQPPEIRTLGSSAFILPCSFNASQGRLAIGSVTWFDE 60

Db 1 MAWMLLLILIMVHPGSCALWVSQPPEIRTLGSSAFILPCSFNASQGRLAIGSVTWFDE 60

QY	61	VPGKEVRNGTPEFRGRGLAPLASSRFLHDHQAELHIRDVRGHDAIYVCRVEVLGLGVGTG	120
Db	61	VPGKEVRNGTPEFRGRGLAPLASSRFLHDHQAELHIRDVRGHDAIYVCRVEVLGLGVGTG	120
QY	121	NGTRLVVEKEHPOLGAGTVLLLRAGFYAVSFLSVAVGSTVYYQK-----CLTWKGP	172
Db	121	NGTRLVVEKEHPOLGAGTVLLLRAGFYAVSFLSVAVGSTVYYQKCHCHMGTHCHSSDGP	180
QY	173	RRQLPAVVPAPLPP	186
Db	181	R----GVIPERCP	190
RESULT 5			
ADQ19810	ID	ADQ19810 standard; protein; 190 AA.	
XX	AC	ADQ19810;	
XX	DT	12-AUG-2004 (first entry)	
XX	XX	Human PRO polypeptide #367.	
XX	KW	Human; PRO; immune related disorder; systemic lupus erythematosus;	
KW	KW	rheumatoid arthritis; osteoarthritis; juvenile chronic arthritis;	
KW	KW	systemic sclerosis; Sjogren's syndrome; vasculitis; sarcoidosis;	
KW	KW	autoimmune haemolytic anaemia; autoimmune thrombocytopenia; thyroiditis;	
KW	KW	diabetes mellitus; renal disease; demyelinating disease;	
KW	KW	central nervous system; peripheral nervous system;	
KW	KW	demyelinating polyneuropathy; Guillain-Barre syndrome;	
KW	KW	chronic inflammatory demyelinating polyneuropathy.	
OS	OS	Homo sapiens.	
XX	XX	WO2004043361-A2.	
XX	PD	27-MAY-2004.	
XX	PF	06-NOV-2003; 2003WO-US035268.	
XX	PR	08-NOV-2002; 2002US-0425235P.	
XX	PA	(GETH) GENENTECH INC.	
XX	PI	Pong S, Dennis K, Clark H, Chiu H, Schoenfeld J, Williams PM;	
PI	PI	Wood WI, Wu TD;	
XX	DR	WPI; 2004-420067/39.	
XX	DR	N-PSDB; ADO19809.	
XX	PT	Novel PRO polypeptide e.g., PRO69614, PRO71106, or PRO86388 useful for	
PT	PT	treating an immune related disorder such as systemic lupus erythematosus,	
PT	PT	rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis or	
PT	PT	spondyloarthropathy.	
XX	XX	Claim 7; SEQ ID NO 734; 1731pp; English.	
XX	CC	The invention relates to human PRO polypeptides and the polynucleotides	
CC	CC	encoding them. The polypeptides and polynucleotides are useful for	
CC	CC	treating and diagnosing immune related disorders in mammals. The immune	
CC	CC	related disorders include systemic lupus erythematosus, rheumatoid	
CC	CC	arthritis, osteoarthritis, juvenile chronic arthritis, systemic	
CC	CC	sclerosis, Sjogren's syndrome, vasculitis, sarcoidosis, autoimmune	
CC	CC	haemolytic anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes	
CC	CC	mellitus, immune-mediated renal disease, demyelinating diseases of the	
CC	CC	central or peripheral nervous system, demyelinating polyneuropathy,	
CC	CC	Guillain-Barre syndrome and chronic inflammatory demyelinating	
CC	CC	polyneuropathy. This sequence represents a human PRO polypeptide of the	
XX	XX	invention.	
XX	XX	Sequence 190 AA;	

Query Match	82.1%;	Score 876;	DB 8;	Length 190;	
Best Local Similarity	89.2%;	Pred. No. 5.9e-75;			
Matches 173;	Conservative	2;	Mismatches 7;	Indels 12;	Gaps 2;
QY	1	MAMMLLLILIMVHPGSCALWVSQPPPIRTLEGSSAFLPCSFNASQGRLAIGSVTWFDEV	60		
Db	1	MAMMLLLILIMVHPGSCALWVSQPPPIRTLEGSSAFLPCSFNASQGRLAIGSVTWFDEV	60		
QY	61	VPGKEVRNGTPEFRGRGLAPLASSRFLHDHQAELHIRDVRGHDAIYVCRVEVLGLGVGTG	120		
Db	61	VPGKEVRNGTPEFRGRGLAPLASSRFLHDHQAELHIRDVRGHDAIYVCRVEVLGLGVGTG	120		
QY	121	NGTRLVVEKEHPOLGAGTVLLLRAGFYAVSFLSVAVGSTVYYQK-----CLTWKGP	172		
Db	121	NGTRLVVEKEHPOLGAGTVLLLRAGFYAVSFLSVAVGSTVYYQKCHCHMGTHCHSSDGP	180		
QY	173	RRQLPAVVPAPLPP	186		
Db	181	R----GVIPERCP	190		
RESULT 6					
ADQ30923	ID	ADQ30923 standard; protein; 190 AA.			
XX	AC	ADQ30923;			
XX	DT	23-SEP-2004 (first entry)			
XX	DE	Human NKp30 polypeptide.			
XX	KW	Natural killer cell; NK cell; NKp30; cytostatic; antimicrobial.			
XX	OS	Homo sapiens.			
XX	FT	Key	Location/Qualifiers		
FT	FT	Region	19..138		
FT	FT	/label= Extracellular region	/note= "Region specifically described in Claim 3"		
FT	FT	Region	20..33		
FT	FT	/label	/note= "Immunogenic peptide specifically described in Claim 3"		
FT	FT	Region	139..157		
FT	FT	/label= Transmembrane region	/note= "Region specifically described in Claim 3"		
FT	FT	Region	158..190		
FT	FT	/label= Cytoplasmic tail	/note= "Region specifically described in Claim 3"		
XX	PN	WO2004056392-A1.			
XX	PD	08-JUL-2004.			
XX	PF	22-DEC-2003; 2003WO-EP014716.			
XX	PR	23-DEC-2002; 2002US-0435344P.			
XX	PA	(INNA-) INNATE PHARMA.			
XX	PI	Romagne F, Andre P;			
XX	DR	WPI; 2004-507595/48.			
PT	PT	Pharmaceutical compositions that stimulate proliferation of natural			
PT	PT	killer cells useful for therapy of melanoma, chronic myeloid, and			
PT	PT	leukemia, comprise an anti-natural killer cell receptor antibody and			
PT	PT	interleukins.			
XX	XX	Claim 3; SEQ ID NO 1; 35pp; English.			
XX	CC	The present sequence is that of human NKp30, a 190 amino acid polypeptide			
CC	CC	(about 30 kDa on SDS-PAGE) that is selectively expressed by natural			

20-MAY-1999.
05-NOV-1998; 98WO-US023826.
07-NOV-1997; 97US-0064761P.
(BIOJ) BIOGEN INC.
Browning J;
WPI: 1999-418423/35.
N-PSDB; AAX59347.
Novel B-cell myelin oligodendrocyte glycoproteins.
Claim 2; Page 42; 43pp; English.

This sequence represents human BMOG, a novel member of the B cell myeloma oligodendrocyte glycoprotein family that is expressed by germinal centre B cells. 3 C-terminal splice variants (see AAY06401-03) of BMOG were identified. The protein is present primarily in the spleen, in lymph nodes and in germinal centre B cells. It may have immunoregulatory functions, and soluble or chimeric fusion proteins of BMOG may be used to regulate the immune system in autoimmune or inflammatory disease. Vectors comprising BMOG, prokaryotic and eukaryotic host cells, and a method of producing BMOG using these transformed host cells are also provided. BMOG polypeptides can be used for modulating the immune system of a subject or to inhibit signal transduction in a cell expressing BMOG by contacting it with a soluble BMOG protein. The nucleic acid can be used for gene therapy. The protein can also be used to target a toxin, imaging agent or radionuclide to a cell expressing BMOG. (All claimed)

Sequence 190 AA:

```

every Match      81.9%; Score 874; DB 2; Length 190;
1st Local Similarity 88.7%; Pred.No. 9.1e-75;
Matches 172; Conservative 3; Mismatches 7; Indels 12; Gaps 2

1 MAWMLLLILMVHPGSCALWYSQPPEIRLTGSSAFLPCSFNASQRLAIGSVTWFRDEV 60
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1 MAWMLLLILMVHPGSCALWYSQPPEIRLTGSSAFLPCSFNASQRLAIGSVTWFRDEV 60

61 VPGKEVRNGTPEFRGLRLAPLASSRFLDHQELHRIYRVDHDAISIVYCRVEVLGLGVGTG 120
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
61 VPGKEVRNGTPEFRGLRLAPLASSRFLDHQELHRIYRVDHDAISIVYCRVEVLGLGVGTG 120

121 NCTRLVWKEHPQLGAGTVLLLRAGFYAVSFLSVAVGSTVYQKG-----CLTWKGP 172
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
121 NCTRLVWKEHPQLGAGTVLLLRAGFYAVSFLSVAVGSTVYQKGCHCMGTHCHSSDGP 180

173 RROLPAVVPAPLPP 186
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
181 R-----GVIEPRCP 190
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

```

LT 8	
6402	
AAV06402 standard; protein; 177 AA.	
AAV06402;	
20-SEP-1999 (first entry)	
Human B-cell myelin oligodendrocyte glycoprotein BMOG.	
BMOG; B-cell myelin oligodendrocyte glycoprotein; human; signal transduction; immunomodulator; antiinflammatory; autoimmune disease; inflammation; gene therapy; diagnosis.	
Homo sapiens.	
Key	Location/Oalifiers

FT Peptide 1. .12
FT /note= "leader peptide"
FT Protein 13. .177
FT /note= "mature protein"
FT Modified-site 42
FT /note= "N-glycosylated"
FT Modified-site 68
FT /note= "N-glycosylated"
FT Modified-site 121
FT /note= "N-glycosylated"
FT Domain 139. .162
FT /note= "transmembrane domain"
FT Peptide 166. .177
FT /note= "alternatively spliced C-terminal end"
XX
XX WO9923867-A2.
XX
XX 20-MAY-1999.
XX
XX 05-NOV-1998; 98WO-US023826.
XX
XX 07-NOV-1997; 97US-0064761P.
XX (BIOJ) BIOGEN INC.
XX
XX Browning J;
XX
XX WPI; 1999-418423/35.
XX N-PSDB; AAX59348.
XX Novel B-cell myelin oligodendrocyte glycoproteins.
XX
XX Claim 2; Page 43; 43pp; English.
XX

CC This sequence represents human BMOG, a novel member of the B cell myelin
CC oligodendrocyte glycoprotein family that is expressed by germinal centre
CC B cells. 3 C-terminal splice variants (see AAY06401-03) of BMOG were
CC identified. The protein is present primarily in the spleen, in lymph
CC nodes and in germinal centre B cells. It may have immunoregulatory
CC functions, and soluble or chimeric fusion proteins of BMOG may be used to
CC regulate the immune system in autoimmune or inflammatory disease. Vectors
CC comprising BMOG, prokaryotic and eukaryotic host cells, and a method of
CC producing BMOG using these transformed host cells are also provided. BMOG
CC polypeptides can be used for modulating the immune system of a subject or
CC to inhibit signal transduction in a cell expressing BMOG by contacting it
CC with a soluble BMOG protein. The nucleic acid can be used for gene
CC therapy. The protein can also be used to target a toxin, imaging agent or
CC radionuclide to a cell expressing BMOG. (All claimed)
XX
XX SQ Sequence 177 AA;

Query Match 80.5%; Score 859; DB 2; Length 177;
Best Local Similarity 100.0%; Pred. No. 2.2e-73;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAMWLLILIMVHPGSCALWVSQPPEIRTLGSSAFLLPCSFNASQGRLAIGSVTFWFRDEV 60
Db 1 MAMWLLILIMVHPGSCALWVSQPPEIRTLGSSAFLLPCSFNASQGRLAIGSVTFWFRDEV 60
Qy 61 VPGKEVRNGTPEFRGRPLAPLASSRFLDHQAEHLHIRDVGRGHDSIYVCRVEVLGLGVGTG 120
Db 61 VPGKEVRNGTPEFRGRPLAPLASSRFLDHQAEHLHIRDVGRGHDSIYVCRVEVLGLGVGTG 120
Qy 121 NGTRLVVEKEHPQLGAGTVLLLRAGFYAVSFSLVAVGSTVYYQOK 165
Db 121 NGTRLVVEKEHPQLGAGTVLLLRAGFYAVSFSLVAVGSTVYYQOK 165

RESULT 9
ADY16598
ID ADY16598 standard; protein; 177 AA.
XX
XX AC ADY16598;

XX 05-MAY-2005 (first entry)
XX PRO polypeptide SEQ ID NO 2404.
XX
XX Antiinflammatory; Immune disorder; Dermatological; Immunosuppressive;
XX Antirheumatic; Antiarthritic; Osteopathic; Hemostatic; Antianemic;
XX Antithyroid; Antidiabetic; Nephrotropic; CNS-Gen.; Hepatotropic;
XX Virucide; Gastrointestinal-Gen.; Antipsoriatic; Antiasthmatic;
XX Antiallergic; ds; gene; diagnosis.
XX Homo sapiens.
XX WO2005016962-A2.
XX
XX 24-FEB-2005.
XX
XX 11-AUG-2004; 2004WO-US026249.
XX
XX 11-AUG-2003; 2003US-0493546P.
XX (GETH) GENENTECH INC.
XX Abbas A, Clark H, Ouyang W, Williams MP, Wood WI, Wu TD;
XX WPI; 2005-182330/19.
XX
XX New nucleic acid encoding PRO polypeptide, useful for diagnosing and
XX treating an immune related disorder, e.g. systemic lupus erythematosus,
XX rheumatoid arthritis, osteoarthritis, thyroiditis, or diabetes mellitus.
XX
XX Claim 8; SEQ ID NO 2404; 158pp; English.
XX

CC The invention relates to an isolated nucleic acid encoding a PRO
CC polypeptide. The polypeptide, agonist or an antagonist, antibody,
CC composition, and method are useful for diagnosing and treating an immune
CC related disorder, e.g. systemic lupus erythematosus, rheumatoid
CC arthritis. The present sequence represents a DNA encoding a PRO
CC polypeptide.
XX

SQ Sequence 177 AA;

Query Match 80.5%; Score 859; DB 9; Length 177;
Best Local Similarity 100.0%; Pred. No. 2.2e-73;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAMWLLILIMVHPGSCALWVSQPPEIRTLGSSAFLLPCSFNASQGRLAIGSVTFWFRDEV 60
Db 1 MAMWLLILIMVHPGSCALWVSQPPEIRTLGSSAFLLPCSFNASQGRLAIGSVTFWFRDEV 60
Qy 61 VPGKEVRNGTPEFRGRPLAPLASSRFLDHQAEHLHIRDVGRGHDSIYVCRVEVLGLGVGTG 120
Db 61 VPGKEVRNGTPEFRGRPLAPLASSRFLDHQAEHLHIRDVGRGHDSIYVCRVEVLGLGVGTG 120
Qy 121 NGTRLVVEKEHPQLGAGTVLLLRAGFYAVSFSLVAVGSTVYYQOK 165
Db 121 NGTRLVVEKEHPQLGAGTVLLLRAGFYAVSFSLVAVGSTVYYQOK 165

RESULT 10
AAE19109
ID AAE19109 standard; protein; 135 AA.

XX
XX AAE19109;
XX
XX 21-MAY-2002 (first entry)
XX
XX Human NKp30 protein.
XX
XX Human; natural killer cell activating protein; NKp46; therapy; virucide;
XX viral infection; natural killer cell; NK; NKp44; imaging agent; cancer;
XX detection; carcinoma; melanoma; lymphoma; sarcoma; cytostatic; NKp30.
XX

Human Nkp30 receptor extracellular region sequence.

Human, Nkp30 receptor; natural killer cell; cytostatic; antimicrobial; melanoma; hepatocarcinoma; lung adenocarcinoma; viral infection; tumour; immunosuppressant; antiviral; drug; grafting enhancement; leukaemia; therapy; extracellular region.

Homo sapiens.

WO200136630-A2.

25-MAY-2001.

15-NOV-2000; 2000WO-EP011697.

15-NOV-1999; 99CA-02288307.

15-NOV-1999; 99US-00440514.

(INNA-) INNATE PHARMA SAS.

(UYGE-) UNIV GENOVA.

Moretta A, Bottino C, Biassoni R;

WPI; 2001-329221/34.

Novel compound, useful for detection and/or quantifying the presence of NK cells, comprises the amino acid sequences of the Nkp30 molecule.

Claim 1; Fig 7B; 83pp; English.

The invention relates to human Nkp30 receptor and its corresponding cDNA molecule which is involved in natural cytotoxicity mediated by natural killer (NK) cells and antibodies that identify the same. Nkp30 receptor is a member of immunoglobulin super family (Ig-SF). Nkp30 is selectively expressed on the surface of human mature NK cells. Nkp30 and its cDNA are useful for detecting and/or quantifying the presence of NK cells in a biological sample. The invention also provide kits for detecting and/or quantifying the presence of NK cells, for the selective removal of NK cells from a biological sample, for the positive and selective purification of NK cells from a biological sample and for the in vitro stimulation of NK cell cytotoxicity. The invention further provides a pharmaceutical composition which is used as a drug for grafting enhancement, graft versus host (GVH) inhibition, stimulation of graft versus tumour (GVT) and especially graft versus leukaemia (GvL), and for the prevention, palliation and/or therapy of solid or liquid tumours, such as melanoma, hepatocarcinoma and lung adenocarcinoma, and/or microorganism, notably viral infection. Nkp30 antibodies are useful for identifying Nkp30 natural ligands and allow assessment of the level of surface Nkp30 ligand expressed on an NK-susceptible target cell and the comparison of this level to the standard physiological one. Hence Nkp30 antibodies are useful in the diagnosis of tumours or of infection. The present sequence is the extracellular region of human Nkp30 receptor

Sequence 120 AA;

Query Match 59.2%; Score 632; DB 4; Length 120;
Best Local Similarity 100.0%; Pred. No. 5.4e-52;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

19 LWSQPPEIRTLGGSAFLPCSFNASQGRLAIGSVTWFRDEVVPGKEVRNGTPEFRGLA 78

1 LWSQPPEIRTLGGSAFLPCSFNASQGRLAIGSVTWFRDEVVPGKEVRNGTPEFRGLA 60

79 PLASSRFLHDHQAEHLHVRGHDASIIYVCRVEVLGLGVGTGNGTRLVVEKEHPQLGAGT 138

61 PLASSRFLHDHQAEHLHVRGHDASIIYVCRVEVLGLGVGTGNGTRLVVEKEHPQLGAGT 120

RESULT 13

ADQ30924

ID ADQ30924 standard; protein; 120 AA.

XX AC ADQ30924;

XX

DT 23-SEP-2004 (first entry)

DE Human Nkp30 extracellular region.

XX Natural killer cell; NK cell; Nkp30; cytostatic; antimicrobial.

OS Homo sapiens.

XX WO2004056392-A1.

XX 08-JUL-2004.

XX 22-DEC-2003; 2003WO-EP014716.

XX 23-DEC-2002; 2002US-0435344P.

XX (INNA-) INNATE PHARMA.

XX Romagne F, Andre P;

XX WPI; 2004-507595/48.

Pharmaceutical compositions that stimulate proliferation of natural killer cells useful for therapy of melanoma, chronic myeloid, and leukemia, comprise an anti-natural killer cell receptor antibody and interleukins.

Claim 3; SEQ ID NO 2; 35pp; English.

The present sequence is that of the extracellular region of human Nkp30 ADQ30923, a 190 amino acid polypeptide that is selectively expressed by natural killer (NK) cells, and particularly by mature NK cells. Claimed pharmaceutical compositions that have a stimulating effect on the proliferation of NK cells comprise an antibody such as an anti-Nkp30 antibody or anti-Nkp46 antibody or its immuno-reactive fragment and a cytokine selected from interleukin-2 (IL2), IL12, IL15 and IL21, the antibody(ies) and cytokine(s) being administered together or separately to a subject. The anti-Nkp30 antibody is an isolated antibody or its antigen-binding fragment which specifically binds to Nkp30 or to a fragment, including the extracellular region, of Nkp30. The pharmaceutical compositions, when used for daily subcutaneous injection, comprising from 1 ng to 100 mg/kg (body weight) of antibody(ies), and lower than 1 million units/square meters/day of cytokine(s), are useful for the prevention, palliation and therapy of e.g. melanoma, chronic myeloid leukaemia, acute myeloid leukaemia, lymphoma, multiple myeloma, hepatocarcinoma, lung adenocarcinoma, neuroblastoma and for antimicrobial prevention, palliation and therapy (claimed).

Sequence 120 AA;

Query Match 59.2%; Score 632; DB 8; Length 120;
Best Local Similarity 100.0%; Pred. No. 5.4e-52;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

19 LWSQPPEIRTLGGSAFLPCSFNASQGRLAIGSVTWFRDEVVPGKEVRNGTPEFRGLA 78

1 LWSQPPEIRTLGGSAFLPCSFNASQGRLAIGSVTWFRDEVVPGKEVRNGTPEFRGLA 60

79 PLASSRFLHDHQAEHLHVRGHDASIIYVCRVEVLGLGVGTGNGTRLVVEKEHPQLGAGT 138

61 PLASSRFLHDHQAEHLHVRGHDASIIYVCRVEVLGLGVGTGNGTRLVVEKEHPQLGAGT 120

RESULT 14

ADP48750

ID ADP48750 standard; protein; 382 AA.

XX AC ADP48750;

XX 09-SEP-2004 (first entry)

XX Human Nkp30-Fc conjugate protein SEQ ID NO:12.

membrane-associated biomolecule is selected from a glycosaminoglycan and a proteoglycan. The antibody is capable of blocking the binding of NK cells via NCR to membrane-associated sulfated polysaccharide biomolecules in a cell, therefore, inhibiting NCR-dependent cell lysis associated with autoimmunity. The peptides and antibodies of the invention are useful for targeting a tumor cell in a subject via an NCR-dependent mechanism. The composition and methods of the invention are useful for targeting tumor cells to diagnose and/or treat benign and malignant tumors or proliferative diseases. This sequence represents a fusion protein comprising human CD5 leader sequence and human Nkp30 D domain fused to the FC domain of human IgG1.

Search completed: February 27, 2006, 17:59:07
Job time : 189 secs

Result No.	Score	Query Match	Length	DB	ID	Description
1	118	11.1	136	2	B45893	T-cell receptor al
2	117.5	11.0	132	2	A24402	T-cell receptor al
3	117.5	11.0	232	2	S25756	Ig lambda chain -
4	116.5	10.9	223	2	T09536	cytotoxic T-lympho
5	116	10.9	146	2	S28408	T-cell receptor be
6	116	10.9	226	2	A46477	membrane-bound imm
7	115	10.8	223	2	A23063	cytotoxic T-lympho
8	113	10.6	233	2	S25747	Ig lambda chain -
9	110	10.3	223	2	I46696	CTLA-4 precursor -
10	110	10.3	235	2	S25749	Ig lambda chain -
11	107.5	10.1	138	2	C27577	T-cell receptor al
12	106.5	10.0	131	2	D24092	T-cell receptor al
13	106.5	10.0	131	2	E24092	T-cell receptor al
14	106	9.9	132	1	RWMSAV	T-cell receptor al
15	105	9.8	131	2	F45893	T-cell receptor al
16	104.5	9.8	132	2	S09713	Ig lambda chain V
17	103	9.7	129	2	A43692	T-cell receptor al
18	103	9.7	235	2	S14675	Ig lambda chain -
19	102.5	9.6	110	2	B24092	T-cell receptor al
20	101.5	9.5	139	2	S36325	T-cell receptor de
21	101	9.5	120	2	I54487	T-cell receptor al
22	101	9.5	186	2	S08614	cytotoxic T-lympho
23	100.5	9.4	236	2	S25746	Ig lambda chain -
24	100.5	9.4	1694	2	S50065	sialoadhesin - mou
25	100	9.4	110	2	A24092	T-cell receptor al
26	99.5	9.3	271	2	A53268	T-cell receptor al
27	99	9.3	130	2	A31211	T-cell receptor al
28	98.5	9.2	128	2	S24319	Ig lambda chain pr
29	98.5	9.2	152	2	S21826	T-cell receptor be

C; Superfamily: immunoglobulin V region; immunoglobulin homology

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

Query Match 11.0%; Score 117.5; DB 2; Length 132;
Best Local Similarity 30.8%; Pred. No. 0.0039;
Matches 44; Conservative 17; Mismatches 47; Indels 35; Gaps 9;

QY 12 VHPGSCALW-----VSOPPE-IRTLGSSAFPLPCSFNASQGRLAIGSVTWFRDE 59
DB 3 LHVSLVFLWLQGVSVQKQVQSPESLIYVPEGAMVSLNCSFSDS-----ASQSIWVYQQH 58
QY 60 VVPGKEVR-----NGTPEFRGLAPLASSRFLHDHQAELHIRDVRGHDASIVYVCRVEV 112
DB 59 --PGKPKALISIFSNKK-EGRLTVYLNRAHLH---VSLHIKQSPSDSAVYLCAVRR 112
QY 113 LGLGVGT---GNGTRLVVEKEHP 132
DB 113 SGANTGKLTFGHGTLIRV---HP 132

RESULT 3
S25756
Ig lambda chain - human
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S25756
R;Combiarto, G.; Klobeck, H.G.
Eur. J. Immunol. 21, 1513-1522, 1991
A;Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin lam
A;Reference number: S16439; MUID:91257162; PMID:1904362
A;Accession: S25756
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-232 <COM>
A;Cross-references: UNIPARC:UPI0000115F04; EMBL:X57821; NID:g33741; PIDN:CAA40958.1; PID
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;147-215/Domain: immunoglobulin homology <IMM>

Query Match 11.0%; Score 117.5; DB 2; Length 232;
Best Local Similarity 24.7%; Pred. No. 0.0072;
Matches 53; Conservative 27; Mismatches 74; Indels 61; Gaps 10;

QY 1 MAMMLLLILIMVH-PGSCALMW-SQPEIRTLGSSAFPLPCSFNASQGRLAIGSVTWFRD 58
DB 1 MAWTVLLGLLCHCTGTSVTLTPQPSVAPGKTASITCGN----NIGSKSVHWYQQ 56
QY 59 EVVPGK-----EVRNGTPE-FRGLAPLASSRFLHDHQAELHIRDVRGHDASIVY 107
DB 57 K--PGQAPVLYVYDSDRPSGIPERFSGNS-----GNTATLTISRVEAGDEADYY 105
QY 108 CHVEVLGLGVGNGTRLVW-----EKEHPQLGAGTVLLLRAGFY--AVS 150
DB 106 CQWDSDDVVFGGTKTLVLQPKAAPSVTLFPSPSSBELQANKATLVCLISDFYPGAVT 165
QY 151 FLSVAVGSTVYVYQGGKLTWKGPRRLQPAVVVPAPLP 185
DB 166 -----VAMKADSPVKAGVETTP 184

RESULT 4
T09536
cytotoxic T-lymphocyte protein 4 - human
C;Species: Homo sapiens (man)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
C;Accession: T09536
R;Harper, K.; Balzano, C.; Rouvier, E.; Mattei, M.G.; Luciani, M.F.; Golstein, P.
J. Immunol. 147, 1037-1044, 1991
A;Title: CTLA-4 and CD28 activated lymphocyte molecules are closely related in both mouse
A;Reference number: I49584; MUID:91318145; PMID:1713603
A;Accession: T09536
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-223 <HAR>
A;Cross-references: UNIPARC:UPI0000113991; EMBL:L15006; NID:g291928; PIDN:AA59385.1; PI
C;Genetics:

A;Gene: CTLA4
A;Map position: 2q33
C;Superfamily: T-cell surface glycoprotein CD28; immunoglobulin homology
C;Keywords: T-cell; transmembrane protein

Query Match 10.9%; Score 116.5; DB 2; Length 223;
Best Local Similarity 27.0%; Pred. No. 0.0084;
Matches 54; Conservative 24; Mismatches 93; Indels 29; Gaps 7;

QY 6 LLLIMVHFGSC-ALWVSQPPPIRTLEGSSAFPLPCSFNASQGRLAIGSVTWFRDEVVPGK 64
DB 24 LLFLLFLFVFCCKMEVQAQPAVVLASSRGIASFVCEY-ASPGKATVRVTVLRQADSQVT 82
QY 65 EVRNGTPEFRGLAPLASSRFLHD-----HQAELHIRDVRGHDASIVYVCRVVL-- 113
DB 83 EVCAATYMTGNELT-----FLDSSICTGSSGNQVNLTIQGLRAMDTGLIYICKVELMYP 136
QY 114 -GLGVGTGNGTRLVVEKEHPQLGAGTVLLLR-----GFVAVSFLSVAVGSVTVYQKCLT 168
DB 137 PPVYLGINGGTQIYVIDPEPCPDSDFLMLLAAVSSGLFFYSFLLTAVSL-----KMLK 191
QY 169 WKGPRLQPAVVVPAPLPPPC 188
DB 192 KRSLPTTGVVYVVKMPTEPEC 211

RESULT 5
S26408
T-cell receptor beta chain V region (5.5) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C;Accession: S26408
R;Bowman, S.J.; Lanchbury, J.S.
submitted to the EMBL Data Library, September 1992
A;Description: T cell receptor beta chain sequences from patients with rheumatoid arthri
A;Reference number: S26408
A;Accession: S26408
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-146 <BOW>
A;Cross-references: UNIPARC:UPI0000116077; EMBL:X68527; NID:g36172; PIDN:CAA48540.1; PID
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: T-cell receptor
F;35-112/Domain: immunoglobulin homology <IMM>

Query Match 10.9%; Score 116; DB 2; Length 146;
Best Local Similarity 26.5%; Pred. No. 0.0058;
Matches 39; Conservative 26; Mismatches 52; Indels 30; Gaps 7;

QY 1 MAMMLLLILIMVHFGSCALMWVSQPE--IRTLGSSAFPLPCSFNASQGRLAIGSVTWFRD 58
DB 6 LCWVLLCLL---GAGSVETGVTQSPTHLIKT-RGQVTLRCSSQSGH-----NTVSWYQQ 56
QY 59 EVVPG-----KEVRNGTPEFRGLAPLASSRFLHDHQAELHIRDVRGHDASIVYVCRV 110
DB 57 ALGQGPQPIFOYREENG-----RGNFPFRSGLOFPNYSSELNVNLELDDSDALYLCA 112
QY 111 EVLGLGVGT-----GNGTRLVVEKE 130
DB 113 SPKGLGLPSRGVEQYFGGTLTVED 139

RESULT 6
A46477
membrane-bound immunoglobulin Ig-alpha chain precursor - human
N;Alternate names: B-cell antigen receptor complex alpha chain CD79a; IgM-alpha; immunog
C;Species: Homo sapiens (man)
C;Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
A;Accession: I54539; A46477; A49135; A46479; I54496; I57851; S51113
R;Hashimoto, S.; Mohrenweiser, H.W.; Gregersen, P.K.; Chlorazzi, N.
Immunogenetics 40, 287-295, 1994
A;Title: Chromosomal localization, genomic structure, and allelic polymorphism of the hu
A;Reference number: I54539; MUID:94364636; PMID:7916003

Query Match

C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S25747
R;Combrriato, G.; Klobeck, H.G.
Eur. J. Immunol. 21, 1513-1522, 1991
A;Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin lambda
A;Reference number: S16439; MUID:91257162; PMID:1904362
C;Accession: S25747
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-233 <COM>
A;Cross-references: UNIPARC:UPI0000115BFD; EMBL:X57812; NID:G33723; PIDN:CAA40949.1; PID
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
P;148-216/Domain: immunoglobulin homology <IMM>

Query Match 10.6%; Score 113; DB 2; Length 233;
Best Local Similarity 26.0%; Pred. No. 0.018;
Matches 56; Conservative 27; Mismatches 72; Indels 60; Gaps 12;

QY 1 MAWMLLLIMVH-PGSCALWV-SOPPEIRTLGSSAFPLPCSFNASQ-RLAIGSVTWFR 57
DB 1 MAWVLLGLLCHTGVSTVSLTPPESVSVAPKAARITCG-----GINTASKSVHWYQ 55
QY 58 DE-----VVPQKEVR-NGTPE-FRGRPLASSRFLHDHQAELHIRDVRGHDASIYVC 108
DB 56 QKPGQAPVLVVGSDRPSGIPERFSGNS-----GNTATLINISRVEAGDEAAYC 106
QY 109 RV-EVLGLGVGTNGTRLV-----EKEHPQLGAGTVLLLRAGFY--AVS 150
DB 107 QVWDSSSDHVVFGGTKLTVLQPKAAPSVTLFPPSSSEELQANKATLVCLISDFYPGAVT 166
QY 151 FLSVAVGTVVYVGKCLTWKGRQLPAVVPAPLP 185
DB 167 -----VAVKADSSPVKAGVETTP 185

RESULT 9
146696
CTLA-4 precursor - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 14-Feb-1997 #sequence_revision 14-Feb-1997 #text_change 09-Jul-2004
C;Accession: I46696
R;Iseno, T.; Seto, A.
Immunogenetics 42, 217-220, 1995
A;Title: Cloning and sequencing of the rabbit gene encoding T-cell costimulatory molecu
A;Reference number: I46689; MUID:95369849; PMID:7642234
C;Accession: I46696
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-223 <ISO>
A;Cross-references: UNIPROT:P42072; UNIPARC:UPI0000012862A; GB:D49844; NID:G755100; PIDN:
C;Superfamily: T-cell surface glycoprotein CD28; immunoglobulin homology

Query Match 10.3%; Score 110; DB 2; Length 223;
Best Local Similarity 26.9%; Pred. No. 0.031;
Matches 52; Conservative 24; Mismatches 101; Indels 16; Gaps 5;

QY 6 LLILIMVHPCALWVSOPPEIRTLGSSAFPLPCSFNASQRLAIGSVTWFRDEVVPCKE 65
DB 25 LFSLLFLVFSKALHVSQPAVVLASSRGVASFVCEY-ASSHKATEVTVTLRQANSQMT 83
QY 66 VRNGTPEFRGRPLASSR---FLHDHQAELHIRDVRGHDASIYVCRVEVL---GLGVGT 119
DB 84 VCAMTYTVENELTFIDSTCTGISHGNKVNLTIOGLSAMDTGLYICKVELMYPPPYVGM 143
QY 120 GNGTRLVVEKEHPQLGAGTVLLRA-----GFIYAVSFLSVAVGTVVYVGKCLTWKGRPRQ 175
DB 144 GNGTQIVVIEPEPCDSDFLILWILAAISSGLFFYSFLITAVLSL-----KMLKKRSLPT 198
QY 176 LPAVVPAPLPPPC 188
DB 199 GVIYKMPTEPEC 211

C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S25749
R;Combrriato, G.; Klobeck, H.G.
Eur. J. Immunol. 21, 1513-1522, 1991
A;Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin lambda
A;Reference number: S16439; MUID:91257162; PMID:1904362
C;Accession: S25749
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-235 <COM>
A;Cross-references: UNIPARC:UPI0000115BFD; EMBL:X57814; NID:G33727; PIDN:CAA40951.1; PID
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
P;150-218/Domain: immunoglobulin homology <IMM>

Query Match 10.3%; Score 110; DB 2; Length 235;
Best Local Similarity 23.7%; Pred. No. 0.032;
Matches 52; Conservative 29; Mismatches 72; Indels 66; Gaps 12;

QY 1 MAWMLLLIMVHPGS---CALWVSOPPEIRTLGSSAFPLPCSFNASQRLAIGSVTWFR 57
DB 1 MAWMLLLGLLAY-GSGVDSQTVTQEPFSFMSPGGTVTLTCGLSSGSGSTSY-SFSWYQ 58
QY 58 DEVVPQKEVR-----NGTPE-FRGRPLASSRFLHDHQAELHIRDVRGHDASIY 106
DB 59 Q--TPQAPRTLMYNTNTRSSGVDPDFSGSIL-----GNKSALTITGAQAEESDY 107
QY 107 VCRVEVLGLGVGT---GNGTRLV-----EKEHPQLGAGTVLLLRAGFY- 147
DB 108 YC---VLYMGRGIVIFGGTKLTVLQPKAAPSVTLFPPSSSEELQANKATLVCLISDFYP 164
QY 148 -AVSFLSVAVGTVVYVGKCLTWKGRQLPAVVPAPLP 185
DB 165 GAVT-----VAVKADSSPVKAGVETTP 187

RESULT 11
C27577
T-cell receptor alpha chain V region (5/10-20D) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 30-May-1997
C;Accession: C27577; C27557
R;Iwamoto, A.; Ohashi, P.S.; Pircher, H.; Walker, C.L.; Michalopoulos, E.E.; Rupp, F.; H;
J. Exp. Med. 165, 591-600, 1987
A;Title: T cell receptor variable gene usage in a specific cytotoxic T cell response. Pr
A;Reference number: A27557; MUID:87139812; PMID:3493320
C;Accession: C27577
A;Molecule type: mRNA
A;Residues: 1-138 <IWA>
A;Cross-references: UNIPARC:UPI00001768DB
A;Accession: C27557
A;Molecule type: mRNA
A;Residues: 22-138 <IW2>
A;Cross-references: UNIPARC:UPI00001768DB; EMBL:X05733
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: T-cell receptor

Query Match 10.1%; Score 107.5; DB 2; Length 138;
Best Local Similarity 31.9%; Pred. No. 0.03;
Matches 38; Conservative 17; Mismatches 45; Indels 19; Gaps 7;

QY 21 VSOPPE-IRTLGSSAFPLPCSFNASQRLAIGSVTWFRDEVVPQKEVR-----NGTPE 72
DB 24 VQSPESLIVPEGAMTSLNCTFSDSASQY----FAWYRQH--SGKAPKALMSIFSNGEKE 77
QY 73 FRGRPLASSRFLHDHQAELHIRDVRGHDASIYVCRVEVL-GLGVGTNGTRLVVEKE 130

Db 78 -EGRFTIHLNKASLH---FSLHIRDSPQSDSALYLCAVSMGGYKVFSGTRLIVSPD 132

RESULT 12

D24092

T-cell receptor alpha chain precursor V region (B10) - mouse

C:Species: Mus musculus (house mouse)

C:Date: 19-Nov-1988 #sequence_revision 01-Dec-2000 #text_change 11-Jan-2002

C:Accession: D24092; S03507

R:Fink, P.J.; Mattis, L.A.; McElligott, D.L.; Bookman, M.; Hedrick, S.M.

Nature 321, 219-226, 1986

A:Title: Correlations between T-cell specificity and the structure of the antigen receptor

A:Reference number: A93380; MUID:86230843; PMID:3012351

A:Accession: D24092

A:Molecule type: mRNA

A:Residues: 1-131 <FTN>

A:Cross-references: UNIPARC:UPI0000176EBD

R:Winoto, A.; Mjølness, S.; Hood, L.

Nature 316, 832-836, 1985

A:Title: Genomic organization of the genes encoding mouse T-cell receptor alpha-chain.

A:Reference number: S03503; MUID:85296332; PMID:2993908

A:Accession: S03507

A:Molecule type: DNA

A:Residues: 111-130 <WIN>

A:Cross-references: UNIPARC:UPI0000115274; EMBL:X03057; NID:G54519; PIDN:CAA26864.1; PIDN:CAA26864.1; PIDN:CAA26864.1

A:Note: this sequence was determined from the germline gene

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: T-cell receptor

F:1-20/Domain: signal sequence #status predicted <SIG>

F:21-131/Product: T-cell receptor alpha chain V region B10 #status predicted <MAT>

F:36-109/Domain: immunoglobulin homology <IMW>

Query Match 10.0%; Score 106.5; DB 2; Length 131;

Best Local Similarity 29.6%; Pred. No. 0.034;

Matches 37; Conservative 19; Mismatches 42; Indels 27; Gaps 7;

Qy 21 VSQPEIRTL-EGSAFLPCSFNASQGLAIGSVTWTF----RDEVVPGKEVRNGTPPERG 75

Db 24 VEQSPSALSLEHGTSALRCNFTTT-----MRAVQWFKNSGSLINLFYLSAGTKE-NG 77

Qy 76 RLAPLASSRFLHDHQAELHIRDVGRGHDSIYVCRVEVLGLGVGTGNGTRLVVEKEHPOLG 135

Db 78 RLKSAFDSK---ERYSTLHIRDAQLEDSTGYFCAAE-----ATSSGOKLV-----FG 121

Qy 136 AGTVL 140

Db 122 QGTIL 126

RESULT 13

T-cell receptor alpha chain precursor V region (4.C3) - mouse

C:Species: Mus musculus (house mouse)

C:Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 21-Jan-2000

C:Accession: E24092

R:Fink, P.J.; Mattis, L.A.; McElligott, D.L.; Bookman, M.; Hedrick, S.M.

Nature 321, 219-226, 1986

A:Title: Correlations between T-cell specificity and the structure of the antigen receptor

A:Reference number: A93380; MUID:86230843; PMID:3012351

A:Accession: E24092

A:Molecule type: mRNA

A:Residues: 1-131 <FTN>

A:Cross-references: UNIPARC:UPI0000176E34

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: T-cell receptor

F:1-20/Domain: signal sequence #status predicted <SIG>

F:21-131/Product: T-cell receptor alpha chain V region 4.C3 #status predicted <MAT>

F:36-109/Domain: immunoglobulin homology <IMW>

Query Match 10.0%; Score 106.5; DB 2; Length 131;

Best Local Similarity 29.6%; Pred. No. 0.034;

Matches 37; Conservative 19; Mismatches 42; Indels 27; Gaps 7;

Qy 21 VSQPEIRTL-EGSAFLPCSFNASQGLAIGSVTWTF----RDEVVPGKEVRNGTPPERG 75

Db 24 VEQSPSALSLEHGTSALRCNFTTT-----MRAVQWFKNSGSLINLFYLSAGTKE-NG 77

Qy 76 RLAPLASSRFLHDHQAELHIRDVGRGHDSIYVCRVEVLGLGVGTGNGTRLVVEKEHPOLG 135

Db 78 RLKSAFDSK---ERYSTLHIRDAQLEDSTGYFCAAE-----STSSGOKLV-----FG 121

Qy 136 AGTVL 140

Db 122 QGTIL 126

RESULT 14

RMSAV

T-cell receptor alpha chain precursor V region (2B4) - mouse

C:Species: Mus musculus (house mouse)

C:Date: 28-May-1986 #sequence_revision 28-May-1986 #text_change 09-Jul-2004

C:Accession: A02015

R:Chien, Y.; Becker, D.M.; Lindsten, T.; Okamura, M.; Cohen, D.I.; Davis, M.M.

Nature 312, 31-35, 1984

A:Title: A third type of murine T-cell receptor gene.

A:Reference number: A93344; MUID:85036634; PMID:6548551

A:Accession: A02015

A:Molecule type: mRNA

A:Residues: 1-132 <CHI>

A:Cross-references: UNIPROT:P01739; UNIPARC:UPI00000270CC

A:Experimental source: hybridoma 2B4, clone TT11

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: Glycoprotein; heterotrimer; receptor; T-cell

F:1-20/Domain: signal sequence #status predicted <SIG>

F:21-132/Product: T-cell receptor alpha chain V region (2B4) #status predicted <MAT>

F:21-113/Region: V segment

F:114-117/Region: D segment

F:118-132/Region: J segment

F:42/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 9.9%; Score 106; DB 1; Length 132;

Best Local Similarity 25.8%; Pred. No. 0.038;

Matches 40; Conservative 22; Mismatches 45; Indels 48; Gaps 9;

Qy 3 WMLLLILIMVHGSCALWVS-----OPPEIRTEGSSAPLPCSFNASQGLAIGSVTW 55

Db 12 WLLIL-----NWVNSQQNVQSPESLIIVPEGARTSLNCTFSDSASQY----FWW 55

Qy 56 FRDEVVPGKEVR-----NGTPEFRGLAPLASSRFLHDHQAELHIRDVGRGHDSIYVC 108

Db 56 YRQH--SGKAPKALMSIFSNGEKE-EGRFTIHLNKASLH---FSLHIRDSPQSDSALYLC 109

Qy 109 RVEVLGLGVGTGNGTRLVVEKEHPOLGAGTVLLLR 143

Db 110 AVTLVG-----GSGNKLI-----FGTGLLSVK 132

RESULT 15

F45993

T-cell receptor alpha chain precursor V region (BTA25) - bovine

C:Species: Bos primigenius taurus (cattle)

C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 20-Jun-2000

C:Accession: F45893

R:Ishiguro, N.; Tanaka, A.; Shinagawa, M.

Immunogenetics 31, 57-60, 1990

A:Title: Sequence analysis of bovine T-cell receptor alpha chain.

A:Reference number: A45893; MUID:90129157; PMID:2137108

A:Accession: F45893

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-131 <ISH>

A:Cross-references: UNIPARC:UPI000011D08D; GB:D90015; NID:G217618; PIDN:BAAL4065.1; PIDN:BAAL4065.1; PIDN:BAAL4065.1

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: T-cell receptor

F:36-109/Domain: immunoglobulin homology <IMW>

Query Match 9.8%; Score 105; DB 2; Length 131;
Best Local Similarity 30.3%; Pred. No. 0.046;
Matches 36; Conservative 23; Mismatches 34; Indels 26; Gaps 8;
Qy 21 VSQPPERTL-EGSSAFPCSFNASQGRLAIGSVTWFRDEVVPKE-----VNRGTPEF 73
Db | | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | :
24 VEQSPSVLSLQEGANSTLRNFSDT-----VDSVQWFQON--PGGALTTLFFFIASGTTK- 75
Qy 74 RGRPLASSRFLHDHQAELHIRDVRGHDAIYVCRVEVLGLGVGT-----GNGTRLVV 127
Db | | : | : | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | :
76 NERMSSTVNSK---ERYSTLHTASQLEDAATYLCAVD---LGSGRQLVFGKGRRLAV 128

Search completed: February 27, 2006, 18:03:48
Job time : 42 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 27, 2006, 17:56:08 ; Search time 230 Seconds
(without alignments)
616.570 Million cell updates/sec

Title: US-10-696-259-6
Perfect score: 1067
Sequence: 1 MAWMLLLILIMVHFGSCALW.....APLPFGSSAHLPPVPG 201

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_05.80.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	DB	ID	Description
1	1067	100.0	201	1	NCTR3_HUMAN	O14931 homo sapien
2	1051	98.5	201	1	NCTR3_PANTR	P61484 pan troglod
3	1018	95.4	201	1	NCTR3_MACMU	Q8nj02 macaca mula
4	826	77.4	176	1	NCTR3_MACFA	P61483 macaca fasc
5	590	55.3	192	1	NCTR3_RAT	Q8cfd9 rattus norv
6	504	47.2	122	2	Q4ZJ77_CANFA	Q4zje7 canis famil
7	136.5	12.8	235	2	Q99M11_MOUSE	Q99m11 mus musculu
8	126	11.8	221	2	Q28090_BOVIN	Q28090 bos taurus
9	124	11.6	221	2	Q97631_SHEEP	O97631 ovis aries
10	123.5	11.6	313	2	Q61PUI_HUMAN	O61pul homo sapien
11	122.5	11.5	234	2	Q6GMW3_HUMAN	Q6gmw3 homo sapien
12	121	11.3	223	2	Q7TMK1_MOUSE	Q7tmk1 mus musculu
13	119	11.2	223	2	Q7JHUO_MACNE	Q7jhu0 macaca neme
14	119	11.2	223	2	Q7JHU2_CERTO	Q7jhj2 cercocebus
15	119	11.2	223	2	Q9BDC4_MACMU	Q9bdc4 macaca mula
16	119	11.2	223	2	Q9BDN7_PAPAN	Q9bdn7 papio anubi
17	118.5	11.1	223	1	CTLA4_HUMAN	P16410 homo sapien
18	118.5	11.1	223	2	Q33TD5_HUMAN	Q33td5 homo sapien
19	118.5	11.1	223	2	Q6GR94_HUMAN	Q6gr94 homo sapien
20	118	11.1	223	2	Q62859_RAT	Q62859 rattus norv
21	117	11.0	223	2	Q6GTR6_MOUSE	Q6gtr6 mus musculu
22	116	10.9	226	1	CD79A_HUMAN	P11912 homo sapien
23	115	10.8	223	1	CTLA4_MOUSE	P09793 mus musculu
24	115	10.8	223	2	Q9GKP2_CANFA	Q9gkp2 canis famil
25	112.5	10.5	234	2	Q6GMV8_HUMAN	Q6gmv8 homo sapien
26	112	10.5	223	2	Q9XSY7_FELCA	Q9xsy7 felis silve
27	112	10.5	223	2	Q9XTAL_FELCA	Q9xtal felis silve
28	112	10.5	700	1	K1RR2_MOUSE	Q7tsu7 mus musculu
29	111	10.4	223	2	Q9JLV3_MARMO	Q9jlv3 marmota mon
30	110	10.3	223	1	CTLA4_FIG	Q9myx7 sus scrofa
31	110	10.3	223	1	CTLA4_RABIT	P42072 oryctolagus

32	110	10.3	223	2	Q9N186_PIG	Q9n186 sus scrofa
33	110	10.3	233	2	Q96I69_HUMAN	Q96i69 homo sapien
34	110	10.3	237	2	Q6DHW4_HUMAN	Q6dhw4 homo sapien
35	109.5	10.3	240	2	Q6MG96_RAT	Q6mg96 rattus norv
36	109	10.2	172	2	Q7LAW3_BOVIN	O7law3 bos taurus
37	109	10.2	223	2	Q9BDP1_AOTTR	Q9bdp1 aotus trivi
38	108.5	10.2	236	2	Q6GMX4_HUMAN	Q6gmx4 homo sapien
39	108.5	10.2	350	2	Q9VFU7_DROME	Q9vfu7 drosophila
40	108.5	10.2	449	2	Q9NKA5_DROME	Q9nka5 drosophila
41	108.5	10.2	867	2	Q59DZ1_DROME	Q59dz1 drosophila
42	108	10.1	387	1	SIG13_PANTR	O64ja4 pan troglod
43	107	10.0	226	2	Q53F88_HUMAN	Q53fb8 homo sapien
44	106.5	10.0	236	2	Q6PIQ7_HUMAN	Q6piq7 homo sapien
45	106	9.9	132	1	TVA2_MOUSE	P01739 mus musculu

ALIGNMENTS

RESULT 1

NCTR3_HUMAN STANDARD; PRT; 201 AA.

AC O14931; O14930; O14932; O95667; O95669; Q5ST90; Q5ST91; Q5ST92; Q5STA3;

DT 05-JUL-2004 (Rel. 44, Created)

DT 05-JUL-2004 (Rel. 44, Last sequence update)

DT 13-SEP-2005 (Rel. 48, Last annotation update)

DE Natural cytotoxicity triggering receptor 3 precursor (Natural killer cell p30-related protein) (Nkp30) (NK-p30).

DE Name=NCR3; Synonyms=IC7;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

OC NCBI_TaxID=9606;

OX [1]

RP NUCLEOTIDE SEQUENCE (ISOFORM 2), TISSUE SPECIFICITY, INTERACTION WITH CD32, AND FUNCTION.

RC TISSUE=Lymphoid;

RA Pende D., Parolini S., Pessino A., Sivori S., Augugliaro R., Morelli L., Marcenaro E., Accame L., Malaspina A., Biassoni R., Bottino C., Moretta L., Moretta A.;

RA "Identification and molecular characterization of Nkp30, a novel triggering receptor involved in natural cytotoxicity mediated by human natural killer cells."

RL J. Exp. Med. 190:1505-1516(1999).

RN [2]

RP NUCLEOTIDE SEQUENCE (ISOFORM 2), TISSUE SPECIFICITY, AND INTERACTION WITH CD32.

RC TISSUE=Periphereal blood;

RA Sato M., Yabe T., Ohashi J., Tsuchiya N., Hanaoka K., Tokunaga K., Juji T.;

RA "Identification of two novel single nucleotide polymorphisms in the Nkp30 gene in human natural killer cells."

RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.

RN [3]

RP NUCLEOTIDE SEQUENCE (ISOFORMS 1; 2; 3; 4; 5 AND 6).

RA MEDLINE=99218514; PubMed=10202016;

RA Neville M.J., Campbell R.D.;

RA "A new member of the Ig superfamily and a V-ATPase G subunit are among the predicted products of novel genes close to the TNF locus in the human MHC."

RL J. Immunol. 162:4745-4754(1999).

RN [4]

RP NUCLEOTIDE SEQUENCE (ISOFORMS 1; 2 AND 3).

RC TISSUE=Spleen;

RA MEDLINE=96422187; PubMed=8824804; DOI=10.1006/geno.1996.0034;

RA Nalabolu S.R., Shukla H., Nallur G., Parimoo S., Weissman S.M.;

RA "Genes in a 220-kb region spanning the TNF cluster in human MHC."

RL Genomics 31:215-222(1996).

RN [5]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

DR EMBL; BC052582; AAH52582.1; -: mRNA.
 DR HGNC; HGNC:19077; NCR3.

Query Match 100.0%; Score 1067; DB 1; Length 201;
 Best Local Similarity 100.0%; Pred. No. 1.6e-83;
 Matches 201; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAMMLLILIMVHPGSCALWVSQPPEIRLTLEGSSAFILPCSFNASQGRLAIGSVTWRDEV 60
 Db 1 MAMMLLILIMVHPGSCALWVSQPPEIRLTLEGSSAFILPCSFNASQGRLAIGSVTWRDEV 60

Qy 61 VPKKEVRNGTPEFRGLAPLASSRFLHDHQAELHIRDVRGHDASIIYVCRVEVLGLGVGTG 120
 Db 61 VPKKEVRNGTPEFRGLAPLASSRFLHDHQAELHIRDVRGHDASIIYVCRVEVLGLGVGTG 120

Qy 121 NGTRLVVEKEHPQLGAGTVLLLRAGFYAVSFLSVAVGSTVYYQKCLTWKGPRLPAVV 180
 Db 121 NGTRLVVEKEHPQLGAGTVLLLRAGFYAVSFLSVAVGSTVYYQKCLTWKGPRLPAVV 180

Qy 181 PAPLPPCGSSAHLPPVPGG 201
 Db 181 PAPLPPCGSSAHLPPVPGG 201

RESULT 2
 NCTR3_PANTR STANDARD; PRT; 201 AA.

AC P61484;
 DT 05-JUL-2004 (Rel. 44, Created)
 DT 05-JUL-2004 (Rel. 44, Last sequence update)
 DE Natural cytotoxicity activating receptor 3 precursor (Natural killer
 DE cell p30-related protein) (Nkp30) (NK-p30).
 DE Name=NCR3;
 GN Pan troglodytes (Chimpanzee).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Pan.
 OX NCBI_TaxID=9598;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Lymphoid;
 RA Blassoni R.;
 RT "Characterization of natural killer receptors in chimpanzees.";
 RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Cytotoxicity activating receptor that may contribute to
 CC the increased efficiency of activated natural killer (NK) cells to
 CC mediate tumor cell lysis (By similarity).
 CC -!- SUBUNIT: Interacts with CD32 (By similarity).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
 CC -!- SIMILARITY: Belongs to the natural cytotoxicity receptor (NCR)
 CC family.
 CC -!- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.

CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.

CC -----
 CC EMBL; AJ516006; CAD56759.1; -: mRNA.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR007110; Ig-like.
 DR SMART; SM00409; IG; 1.
 DR PROSITE; PS00835; IG_LIKE; 1.
 KW Glycoprotein; Immunoglobulin domain; Receptor; Signal; Transmembrane.
 FT SIGNAL 1 18
 FT CHAIN 19 201 Natural cytotoxicity triggering receptor
 FT 3.
 FT TOPO_DOM 19 135 Extracellular (Potential).
 FT TRANSMEM 136 156 Potential.
 FT TOPO_DOM 157 201 Cytoplasmic (Potential).
 FT DOMAIN 19 126 Ig-like.

FT CARBOHYD 42 42 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 121 121 N-linked (GlcNAc...) (Potential).
 FT DISULFID 39 108 By similarity.
 SQ SEQUENCE 201 AA; 21656 MW; 3768ACCT68E8D749 CRC64;

Query Match 98.5%; Score 1051; DB 1; Length 201;
 Best Local Similarity 99.0%; Pred. No. 3.7e-82;
 Matches 199; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MAMMLLILIMVHPGSCALWVSQPPEIRLTLEGSSAFILPCSFNASQGRLAIGSVTWRDEV 60
 Db 1 MAMMLLILIMVHPGSCALWVSQPPEIRLTLEGSSAFILPCSFNASQGRLAIGSVTWRDEV 60

Qy 61 VPKKEVRNGTPEFRGLAPLASSRFLHDHQAELHIRDVRGHDASIIYVCRVEVLGLGVGTG 120
 Db 61 VPKKEVRNGTPEFRGLAPLASSRFLHDHQAELHIRDVRGHDASIIYVCRVEVLGLGVGTG 120

Qy 121 NGTRLVVEKEHPQLGAGTVLLLRAGFYAVSFLSVAVGSTVYYQKCLTWKGPRLPAVV 180
 Db 121 NGTRLVVEKEHPQLGAGTVLLLRAGFYAVSFLSVAVGSTVYYQKCLTWKGPRLPAVV 180

Qy 181 PAPLPPCGSSAHLPPVPGG 201
 Db 181 PAPLPPCGSSAHLPPVPGG 201

RESULT 3
 NCTR3_MACMU STANDARD; PRT; 201 AA.

ID NCTR3_MACMU STANDARD; PRT; 201 AA.
 AC Q8MJ02; Q8MJ02; Q8MJ00; Q8MJ01; Q95JB8;
 DT 05-JUL-2004 (Rel. 44, Created)
 DT 10-MAY-2005 (Rel. 47, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Natural cytotoxicity triggering receptor 3 precursor (Natural killer
 DE cell p30-related protein) (Nkp30) (NK-p30).
 DE Name=NCR3;
 GN Macaca mulatta (Rhesus macaque).
 OS Macaca mulatta (Rhesus macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 OC Cercopitheidae; Cercopitheciae; Macaca.
 OX NCBI_TaxID=9544;
 RN [1]
 RP NUCLEOTIDE SEQUENCE (ISOFORMS 1; 2; 3 AND 4), AND VARIANT VAL-156.
 RA LaBonte M.L., Miller J., Letwin N.L.;
 RT "Molecular cloning of rhesus monkey Nkp46 and Nkp30 and identification
 RT of Nkp46SD and Nkp30S.";
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 CC [2]
 RN NUCLEOTIDE SEQUENCE (ISOFORMS 1 AND 4), AND VARIANT VAL-156.
 RC TISSUE=Lymphoid;
 RA Rizzi M., Blassoni R.;
 RT "NCR express by macaca NK cells.";
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA] (ISOFORM 5).
 RP PubMed=15269276; DOI=10.1093/molbev/meh216;
 RA Kulski J.K., Anzai T., Shiina T., Inoko H.;
 RT "Rhesus macaque class I duplicon structures, organization, and
 RT evolution within the alpha block of the major histocompatibility
 RT complex.";
 RL Mol. Biol. Evol. 21:2079-2091(2004).
 CC -!- FUNCTION: Cytotoxicity activating receptor that may contribute to
 CC the increased efficiency of activated natural killer (NK) cells to
 CC mediate tumor cell lysis (By similarity).
 CC -!- SUBUNIT: Interacts with CD32 (By similarity).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=5;
 CC Name=5;
 CC IsoId=Q8MJ02-5; Sequence=Displayed;
 CC Name=1;
 CC IsoId=Q8MJ02-1; Sequence=VSP_013641, VSP_013642;
 CC Note=No experimental confirmation available;

	Name=2;	Isoid-Q8MJ02-2; Sequence=VSP_010414;
	Note=No experimental confirmation available;	
	Name=3;	Isoid-Q8MJ02-3; Sequence=VSP_010415, VSP_010416;
	Note=No experimental confirmation available;	
	Name=4;	Isoid-Q8MJ02-4; Sequence=VSP_010417;
	Note=No experimental confirmation available;	
-!	SIMILARITY:	Belongs to the natural cytotoxicity receptor (NCR) family.
-!	SIMILARITY:	Contains 1 Ig-like (immunoglobulin-like) domain.
This	Swiss-Prot entry is copyright.	It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.
EMBL;	AY035214;	AAK63117.1; -, mRNA.
EMBL;	AY035215;	AAG63117.1; -, mRNA.
EMBL;	AY035216;	AAG63118.1; -, mRNA.
EMBL;	AY035217;	AAG63119.1; -, mRNA.
EMBL;	AJ554301;	CAD86942.1; -, mRNA.
EMBL;	AB128049;	BAD69721.1; -, Genomic DNA.
HSSP;	P16410;	I185.
DR	InterPro;	IPR003599; IG.
DR	InterPro;	IPR007110; IG-like.
DR	SMART;	SM00409; IG; 1.
DR	PROSITE;	PS50835; IG LIKE; 1.
KW	Alternative splicing;	Glycoprotein; Immunoglobulin domain;
KW	Polymorphism;	Receptor; Signal; Transmembrane.
FT	SIGNAL	1 18 Potential.
FT	CHAIN	19 201 Natural cytotoxicity triggering receptor
FT		3.
FT	TOPO_DOM	19 133 Extracellular (Potential).
FT	TRANSMEM	134 154 Potential.
FT	TOPO_DOM	155 201 Cytoplasmic (Potential).
FT	DOMAIN	19 126 Ig-like.
FT	CARBOHYD	42 42 N-linked (GlcNAc .-) (Potential).
FT	CARBOHYD	121 121 N-linked (GlcNAc .) (Potential).
FT	DISULFID	39 108 By similarity.
FT	VARSPLIC	66 90 Missing (in isoform 2).
FT		/FTIG-VSP_010414.
FT	VARSPLIC	112 115 VLGL -> NILS (in isoform 3).
FT		/FTIG-VSP_010415.
FT	VARSPLIC	116 201 Missing (in isoform 3).
FT		/FTIG-VSP_010416.
FT	VARSPLIC	167 180 LTKWGRRRLPAVV -> HCMGTGHCHSDGP (in isoform 1).
FT		/FTid-VSP_013641.
FT	VARSPLIC	177 201 Missing (in isoform 4).
FT		/FTid-VSP_010417.
FT	VARSPLIC	181 201 Missing (in isoform 1).
FT		/FTid-VSP_013642.
FT	VARIANT	156 156 M -> V.
SQ	SEQUENCE	201 AA; AE3A325C8585BA68 CRC64;
Query Match		95.4%; Score 1018; DB 1; Length 201;
Best Local Similarity		95.0%; Pred. No. 2.5e-79;
Matches 191; Conservative		5; Mismatches 5; Indels 0; Gaps 0
QY	1	MANMALLILLIWMHPGSCALMVVSOPPEIRTLGGSAFLPCSFNASQGRLAIGSVTWPRDEV 60
Db	1	MANMALLILLIWMVPGSCLMVVSOPPEIRTLGGSAFLPCSFNASQGRLAIGSVTWPRDEV 60
QY	61	VPGKEVRNGTPTFRGRLLAPLASRSFLHDQAELHIRDVRGDASIIYVCREVVLGVGVTG 120
Db	61	APGKEVRNGTPTFRGRLLAPLSRSSRFLRDQAELHIWDVRGDAGIIYVCREVVLGVGVTG 120
QY	121	NGTELVVEKHEPHQLGAGTVLLLRAGFYAVSFLSVVGSTVIYYQGKCIWKGPBROLPAVV 180


```
Qy 121 NGTRLVVEKEHPQLGAGTGLVLLLRAGFYAVSFLSVAGSVTVYQK 166
Db 121 NGTRLVVEKEHPQLGAGTGLVLLLRAGFYAVSFLSVAGSVTVYQK 166

RESULT 5
NCTR3 RAT STANDARD; PRT; 192 AA.
AC Q8CFD3; Q80WM8; Q8CG11;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Natural cytotoxicity triggering receptor 3 precursor (Natural killer
cell p30-related protein) (NKp30) (NK-p30).
GN Name=Ncr3; Synonyms=1c7;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE, AND VARIANTS VAL-7; VAL-19; VAL-82 AND THR-138.
RC STRAIN=PVG; TISSUE=Natural killer cell;
RX PubMed=12548565; DOI=10.1002/immu.200310008;
RA Backman-Petersson E., Miller J.R., Hollyoake M., Aguado B.,
RA Butcher G.W.;
RT "Molecular characterization of the novel rat NK receptor 1c7.";
RL Eur. J. Immunol. 33:342-351(2003).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Lewis;
RX MEDLINE=22168131; PubMed=12180816; DOI=10.1016/S0966-3274(02)00033-3;
RA Heish C.L., Obara H., Ogura Y., Martinez O.M., Krams S.M.;
RT "NK cells and transplantation.";
RL Transpl. Immunol. 9:111-114(2002).
RN [3]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Brown Norway;
RX PubMed=15060004; DOI=10.1101/gr.1987704;
RA Hurt P., Walter L., Sudbrak R., Klages S., Mueller I., Shiina T.,
RA Inoko H., Lehrach H., Guenther E., Reinhardt R., Himmelbauer H.;
RT "The genomic sequence and comparative analysis of the rat major
histocompatibility complex.";
RL Genome Res. 14:631-639(2004).
CC -!- FUNCTION: Cytotoxicity activating receptor that may contribute to
the increased efficiency of activated natural killer (NK) cells to
mediate tumor cell lysis (By similarity).
CC -!- SUBUNIT: Interacts with CD32 (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC -!- SIMILARITY: Belongs to the natural cytotoxicity receptor (NCR)
family.
CC -!- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
removed.
CC -----
DR EMBL; AJ430418; CAD23066.1; -; mRNA.
DR EMBL; AJ430419; CAD23067.2; -; Genomic DNA.
DR EMBL; AJ430420; CAD23067.2; JOINED; Genomic DNA.
DR EMBL; AY273824; AAP13457.1; -; mRNA.
DR EMBL; BX883046; CAE84000.1; -; Genomic DNA.
DR HSSP; P09793; 1DQT.
DR Ensembl; ENSRNOG0000000854; Rattus norvegicus.
DR RGD; 727881; 1C7.
DR InterPro; IPR003599; Ig.
DR SMART; SM00409; Ig_1.
DR PROSITE; PS50835; IG-LIKE; 1.
KW Glycoprotein; Immunoglobulin domain; Polymorphism; Receptor; Signal;
```

```
KW Transmembrane. 18 Potential.
FT SIGNAL 192 Natural cytotoxicity triggering receptor
FT CHAIN 19 3.
FT TOPO_DOM 19 Extracellular (Potential).
FT TRANSMEM 148 Potential.
FT TOPO_DOM 169 Cytoplasmic (Potential).
FT DOMAIN 19 Ig-like.
FT CARBOHYD 42 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 121 N-linked (GlcNAc...) (Potential).
FT DISULFID 39 By similarity.
FT VARIANT 7 I -> V.
FT VARIANT 19 I -> V.
FT VARIANT 82 A -> V.
FT VARIANT 138 A -> T.
FT CONFLICT 135 A -> V (in Ref. 2).
SQ SEQUENCE 192 AA; 20470 MW; 7FC84FB252D2377 CRC64;

Query Match 55.3%; Score 590; DB 1; Length 192;
Best Local Similarity 64.2%; Pred. No. 1.3e-42;
Matches 115; Conservative 24; Mismatches 32; Indels 8; Gaps 1;

Qy 1 MAMLLILLIMVHPGSCALWVOPPIRTLEGSSAFPCSFNASQGRLAIGSVTFPRDEV 60
Db 1 MAKVLLIVFMVAGSCAIWVSPPEIRAQEGTTASLPCSFNASRGAATWYQDKV 60
Qy 61 VPGKEVRNGTPEFRGLAPLASSRFLHDHQAELHIRDVRGHDAIYVCRVEVLGLGVGTG 120
Db 61 APMELSNVTPGFRGRVASFSAQFIRGHKAGLLIQIDQSHDARIYVCRVEVLGLGVGTG 120
Qy 121 NGTRLVVEKEHPQ-----LGATVLLLRAGFYAVSFLSVAGSVTVYQKCLTWKG 171
Db 121 NGTRLVVEKEPPQQAASNAEPERAAVTSLLLRAGYVALSFLSVATGTVYQKCLCHVG 179

RESULT 6
Q4ZJE7 CANFA
ID Q4ZJE7 CANFA PRELIMINARY; PRT; 122 AA.
AC Q4ZJE7;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE NKp30 (Fragment).
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC Canis.
OX NCBI_TaxID=9615;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Chu R., Lin Y.-C., Wang Y.-S.;
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; DQ003484; AY21817.1; -; mRNA.
FT NON_TER 1
FT NON_TER 122
SQ SEQUENCE 122 AA; 13307 MW; FB14BD6B314279DA CRC64;

Query Match 47.2%; Score 504; DB 2; Length 122;
Best Local Similarity 79.5%; Pred. No. 2e-35;
Matches 97; Conservative 9; Mismatches 16; Indels 0; Gaps 0;

Qy 19 LWSQPPEIRTLLEGSSAFPCSFNASQGRLAIGSVTFPRDEVVPGKEVRNGTPEFRGLA 78
Db 1 LWVFQPEIHTQGTAAFLPCSFNASERKLAIGSVTWYRDKVAPGKEVRNGTPEFRGLA 60
Qy 79 PLASSRFLHDHQAELHIRDVRGHDAIYVCRVEVLGLGVGTGNGTRLVVEKEHPQLGAGT 138
Db 61 PLPSSRFLCDHQAELHIWDIQDCDAGVYVCRVEVLGLGVGTGNGTLLVVEKGPWLCAST 120
Qy 139 VL 140
Db 121 VL 122
```

RESULT 7
Q99MII_MOUSE PRELIMINARY; PRT; 235 AA.
ID Q99MII_MOUSE
AC Q99MII; 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
OS Mus musculus [Mouse].
OC Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
ON NCBI_TaxID=10090;
RX CB1
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Czech II;
CC TISSUE=Mammary tumor metastatized to lung. Tumor arose spontaneously;
CD MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RE Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Reha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahney J., Halton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield V.S.N., Krzyminska M.I., Skalska U., Smalusz D.E.,
RA Schnurch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
NUCLEOTIDE SEQUENCE.
RC STRAIN=Czech II;
CC TISSUE=Mammary tumor metastatized to lung. Tumor arose spontaneously;
CD Strausberg R.;
RE Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC002129; AAA02129.1; -; mRNA.
DR HSSP; P01843; 1UNH.
DR GO; GO:0003823; F:antigen binding; IEA.
DR InterPro; IPRO07110; IG-like.
DR InterPro; IPRO03597; IG cl.
DR InterPro; IPRO03006; IG_MHC.
DR InterPro; IPRO03596; IG_v.
DR Pfam; PF07654; CI-set; I.
DR SMART; SMO0406; IGV; I.
DR PROSITE; PS50835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOW 1.
KW Hypothetical protein; Immunoglobulin domain.
SQ SEQUENCE 235 AA; 25403 MW; 39807BFE6782A3FB CRC64;
Query Match 12.8%; Score 136.5; DB 2; Length 235;
Best Local Similarity 31.2%; Pred. No. 0.0014;
Matches 43; Conservative 25; Mismatches 49; Indels 21; Gaps 7
QY 1 MAWMLLLLILMVH-PGSCA-LWVSPPEITRTLEGSAFLPCSFNAGSLGTCVTFWRD 58
DB 1 MTWAPLLIVFLHLHTGTSCAQVLVTTPSSYSTLSGSTAKLPCL--KASTGNIGDSYNNWYQQ 58
QY 59 -----EVVPQKEVRNG--TPEFGRLAPLASSRFLPHDQAEHLHRDVGRHDASIVYCR 109
DB 59 YMGRSPTNIYGGDLRPSGSDRFSGSIDSSNSAF-----LTIQNVQADDEADYYCQ 111
QY 110 VEVLGLGVGTGNGTRIVL 127

OC Pecora; Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=9309828; PubMed=10380709; DOI=10.1007/s002510050542;
RA Chaplin P.J., Pietrala L.N., Scheerlinck J.P.;
RT "Cloning and sequence comparison of sheep CD28 and CTLA-4.";
RL Immunogenetics 49:583-584(1999).
CC -!- FUNCTION: Not known (By similarity).
CC -!- SUBUNIT: Associates non-covalently with beta-2-microglobulin (By similarity).
DR EMBL; AF092740; AAD04380.1; -; mRNA.
DR HSSP; P16410; 1185.
DR SMR; O97631; 35-159.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR008096; CTLA4.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; Ig; 1.
DR PRINTS; PR01720; CTLANTIGEN4.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS0835; IG LIKE; 1.
KW Immunoglobulin domain.
SQ SEQUENCE 221 AA; 24490 MW; D317B9D5557BA6FB CRC64;

Query Match 11.6%; Score 124; DB 2; Length 221;
Best Local Similarity 26.9%; Pred. No. 0.016;
Matches 52; Conservative 27; Mismatches 98; Indels 16; Gaps 5;

Qy 6 LLILIMVHPGSCALVWSQPPPIRTLEGSSAFPCSFNASQRLAIGSVTWFRDVPKGE 65
Db 23 LFFLLFPVFSKGNVTPPPVVLASSRGVASFCTCEYESS-GKADEVRTVILRKAGIQVTE 81

Qy 66 VRNCTPFRGRGLAPLASSRFL---HDHQAELHIRDVRGHDAIYVCRVEVL---GLGVGT 119
Db 82 VCATGYVEDELTFDSSCGTSGRGNKVNLTIOQLRAMDTGLYVCKVELMYPPTYNGE 141

Qy 120 GNGTRLVVEKEHPQLGAGTVLLLR-----GFYAVSFSLVAVGSTVYQGKCLTWKGRPRQ 175
Db 142 GNGTQIVVIDPEPCPDSDLWILAAVSSGLFFYSFLITAVSLS-----XWMLKRSPLTT 196

Qy 176 LPVVPAPLPPPC 188
Db 197 GVYVMPPTPEPC 209

RESULT 10
Q6IPUL HUMAN
ID Q6IPUL HUMAN PRELIMINARY; PRT; 313 AA.
AC Q6IPUL;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Shenmen C.M., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettaman M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RP [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Blood;
RA Strausberg R.;
RC Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Beta-2-microglobulin is the beta-chain of major
CC histocompatibility complex class I molecules (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).
DR EMBL; BC071724; AAH71724.1; -; mRNA.
DR HSSP; P01850; 1KGC.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00835; IG LIKE; 2.
DR PROSITE; PS0835; IG LIKE; 2.
KW Hypothetical protein; Immunoglobulin domain.
SQ SEQUENCE 313 AA; 34612 MW; BF890C926CE361BC CRC64;

Query Match 11.6%; Score 123.5; DB 2; Length 313;
Best Local Similarity 25.7%; Pred. No. 0.026;
Matches 46; Conservative 26; Mismatches 62; Indels 45; Gaps 8;

Qy 1 MAMMLLLILIMVHPGSCALVWSQPPPE---IRTLEGSSAFPCSFNASQRLAIGSVTWFRD 58
Db 6 LCWALLCLL---GAGSVETGVTQSPHILKT-RGQVTVLCSSQSGH-----NTVSWYQQ 56

Qy 59 EVVPG-----KEVRNGTPEFRGLAPLASSRFLHDHQAELHIRDVRGHDAIYVCRV 110
Db 57 ALGQGPQFIFQYREEENG---RGNFPPRFSGLQFPVSSSLNVALELDDSLALCAS 112

Qy 111 EVLGLGVGT---GNGTRLVW-----EKEHPQLGAGTVLLLRAGFY 147
Db 113 SLGGPGLGETQYFGPGTRLLVLEDLKNVFPPEVAVPEPSAEISHTOKATLVCLATGFY 171

RESULT 11
Q6GMW3 HUMAN
ID Q6GMW3 HUMAN PRELIMINARY; PRT; 234 AA.
AC Q6GMW3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX TISSUE=Primary B-Cells;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Shenmen C.M., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

```

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny K.C., Halse S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Fahay J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitling M., Touchman J.W., Green E.D., Dickinson M.C.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Schnerch A., Schein J.E., Jones S.J.M., Skalska U., Smalius D.E.,
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RC NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073787; AAH73787.1; -; mRNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG.cl.
DR InterPro; IPR003006; IG.MHC.
DR Pfam; PF07654; Cl-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG LIKE; 2.
DR PROSITE; PS00290; IG MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 234 AA; 24653 MW; 53339D4PF0E6B97 CRC64;

Query Match 11.5%; Score 122.5; DB 2; Length 234;
Best Local Similarity 26.3%; Pred. No. 0.023;
Matches 57; Conservative 27; Mismatches 70; Indels 63; Gaps 12;

QY 1 MAWLLILIMVH-PGSCALMV-SQPPEIRLEGSAPLPCSFNASQRLAIGSVTWFRD 58
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 59 E-----VVPGEKVR-NGTPEFRGLAPLASSRFLHDHQAELHIRDVRGHDASIYVCRV 110
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 57 KPGQAPMLVYDDGARPSSIPE---RFGSGAS-----ENTATLTISGVEAGDEADYICQV 108
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 111 -----EVLGLGVGTGNGTRLVW-----EKHPQLGAGTVLLLRAGFY--A 148
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 109 WHGSSEVI---LVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGA 165
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 149 VSFLSVAVGSTVYYQGGKLTWKGPRLQPLPAVVPAPLP 185
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 166 VT-----VAWKADSSPVKAGVETTP 186
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 12
Q7TMX1 MOUSE PRELIMINARY; PRT; 223 AA.
AC Q7TMX1;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Cytotoxic T-lymphocyte-associated protein 4.
GN Name=Ctla4;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.

```

```

RC STRAIN=C57BL/6Ncr; TISSUE=Hematopoietic Stem Cell;
RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heien F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Caplenton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny K.C., Halse S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Fahay J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitling M., Touchman J.W., Green E.D., Dickinson M.C.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Schnerch A., Schein J.E., Jones S.J.M., Skalska U., Smalius D.E.,
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RC NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6Ncr; TISSUE=Hematopoietic Stem Cell;
RA Strausberg R.;
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC052683; AAH52683.1; -; mRNA.
DR HSSP; P09793; 1DQT.
DR SMR; Q7TMX1; 38-154.
DR MGI; MGI:88556; Ctl4.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR InterPro; IPR008096; CTLA4.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR PRINTS; PR01720; CTLANTIGEN4.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS0835; IG LIKE; 1.
KW Immunoglobulin domain.
SQ SEQUENCE 223 AA; 25035 MW; EE8E4C77E6A04549 CRC64;

Query Match 11.3%; Score 121; DB 2; Length 223;
Best Local Similarity 26.6%; Pred. No. 0.029;
Matches 53; Conservative 27; Mismatches 97; Indels 22; Gaps 7;

QY 3 WMLLILIMVHFGSCALMVVSQPPEIRLEGSAPLPCSFNASQRLAIGSVTWFRD---- 58
DB 22 FVALLTLFLPVPSEAIQVTPSVVLASSHGVSFPCEYSPSHNTDEV-RVTVLRQTNDQ 80
QY 59 --EVPGEKVRNGTPEFRGLAPLASSRFLHDHQAELHIRDVRGHDASIYVCRVEVL---- 113
DB 81 MTEVCATTTTEKNTVGFELD--YFPCSGTF-NESRVNLTIQGLRAVDTGLYLCKELMYP 137
QY 114 GLGVGTGNGTRLVVEKEHPQLGAGTVL----LLRAGFVAVSFSLSVAVGSTVYYQGGKLTW 169
DB 138 PVFVGKNGTRIYVIDPEPCPSDFLLWLILVAVSLGLFFYFLVTAVALS-----KMLKK 192
QY 170 KGPRLQPLPAVVPAPLP 188
DB 193 RSLPTTGVYVKMPPTPEPC 211

RESULT 13
Q7JHJ0 MACNE PRELIMINARY; PRT; 223 AA.
AC Q7JHJ0;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE CD152 protein precursor.
GN Name=CTLA-4;
OS Macaca nemestrina (Pig-tailed macaque).

```

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 OC Cercopithecidae; Cercopithecinae; Macaca.
 OX NCBI_TaxID=9545;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=21383618; PubMed=11491535; DOI=10.1007/s002510100322;
 RA Villinger F., Bostik P., Wayne A.E., King C.L., Genain C.P.,
 RA Weiss W.R., Ansari A.A.;
 RT "Cloning, sequencing, and homology analysis of nonhuman primate
 RT Fas/Fas-ligand and co-stimulatory molecules.";
 RL Immunogenetics 53:315-328(2001).
 DR EMBL; AF344854; AAK37537.1; -, mRNA.
 DR HSSP; P16410; 1AH1.
 DR SMR; Q7JHJ0; 37-161.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0006955; P:immune response; IEA.
 DR InterPro; IPR008096; CTLA4.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR003596; Ig v.
 DR PRINTS; PR01720; CTLANTIGEN4.
 DR SMART; SM00409; IG; 1.
 DR SMART; SM00406; IGv; 1.
 KW Signal.
 FT SIGNAL 1 37 Potential.
 SQ SEQUENCE 223 AA; 24683 MW; BDE42248A00398FA CRC64;
 Query Match 11.2%; Score 119; DB 2; Length 223;
 Best Local Similarity 26.7%; Pred. No. 0.044;
 Matches 54; Conservative 25; Mismatches 95; Indels 28; Gaps 6;
 Qy 3 WMLLLILIMVHPGSCALWVSOPPEIRTELEGSSAFPCSFNASQGRLAIGSVTWFRDEVVP 62
 Db 22 YTLFSLFLFIPVFSKAMHVAQPAVVLANSRGIAFVCEY-ASPKATEVVRTVLRQADSQ 80
 Qy 63 GKEVRNGTPEFRGLAPLASSRFLHD-----HQAELHIRDVRGHDAIYVCRVEVL 113
 Db 81 VTEVCAATYMMGNELT-----FLDSDICTGTSSGNQVNLTIQGLRAMDTGLYICKVELM 134
 Qy 114 ---GLGVGTGNGTRLVVEKEHPQLGAGTVLLRA----GFYAVSFSLVAVGSTVYVYQK 166
 Db 135 YPPPYMGINGTQIYVIDPEPCDPSDFLLWILAAVSSGLFFYSFLLTAVSLS-----KM 189
 Qy 167 LTWKGPRLQPAVVPAPLPPEPC 188
 Db 190 LKRSPLTTGVVVKMPPTPEPC 211
 RESULT 14
 ID Q7JHJ2 CERTO PRELIMINARY; PRT; 223 AA.
 AC Q7JHJ2;
 DT 05-JUL-2004 (TRENBLrel. 27, Created)
 DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
 GN CD152 protein precursor.
 GN Name=CTLA-4;
 OS Cercopithecus torquatus atys (Red-crowned mangabey) (Sooty mangabey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 OC Cercopithecidae; Cercopithecinae; Cercocebus.
 OX NCBI_TaxID=9531;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=21383618; PubMed=11491535; DOI=10.1007/s002510100322;
 RA Villinger F., Bostik P., Wayne A.E., King C.L., Genain C.P.,
 RA Weiss W.R., Ansari A.A.;
 RT "Cloning, sequencing, and homology analysis of nonhuman primate
 RT Fas/Fas-ligand and co-stimulatory molecules.";
 RL Immunogenetics 53:315-328(2001).
 DR EMBL; AF344848; AAK37608.1; -, mRNA.
 DR HSSP; P16410; 1AH1.

DR SMR; Q7JHJ2; 37-161.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0006955; P:immune response; IEA.
 DR InterPro; IPR008096; CTLA4.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR003596; Ig v.
 DR PRINTS; PR01720; CTLANTIGEN4.
 DR SMART; SM00409; IG; 1.
 DR SMART; SM00406; IGv; 1.
 KW Signal.
 FT SIGNAL 1 37 Potential.
 SQ SEQUENCE 223 AA; 24683 MW; BDE42248A00398FA CRC64;
 Query Match 11.2%; Score 119; DB 2; Length 223;
 Best Local Similarity 26.7%; Pred. No. 0.044;
 Matches 54; Conservative 25; Mismatches 95; Indels 28; Gaps 6;
 Qy 3 WMLLLILIMVHPGSCALWVSOPPEIRTELEGSSAFPCSFNASQGRLAIGSVTWFRDEVVP 62
 Db 22 YTLFSLFLFIPVFSKAMHVAQPAVVLANSRGIAFVCEY-ASPKATEVVRTVLRQADSQ 80
 Qy 63 GKEVRNGTPEFRGLAPLASSRFLHD-----HQAELHIRDVRGHDAIYVCRVEVL 113
 Db 81 VTEVCAATYMMGNELT-----FLDSDICTGTSSGNQVNLTIQGLRAMDTGLYICKVELM 134
 Qy 114 ---GLGVGTGNGTRLVVEKEHPQLGAGTVLLRA----GFYAVSFSLVAVGSTVYVYQK 166
 Db 135 YPPPYMGINGTQIYVIDPEPCDPSDFLLWILAAVSSGLFFYSFLLTAVSLS-----KM 189
 Qy 167 LTWKGPRLQPAVVPAPLPPEPC 188
 Db 190 LKRSPLTTGVVVKMPPTPEPC 211
 RESULT 15
 ID Q9BDC4 MACMU PRELIMINARY; PRT; 223 AA.
 AC Q9BDC4;
 DT 01-JUN-2001 (TRENBLrel. 17, Created)
 DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)
 DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
 DE CD152 protein precursor.
 GN Name=CTLA-4;
 OS Macaca mulatta (Rhesus macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 OC Cercopithecidae; Cercopithecinae; Macaca.
 OX NCBI_TaxID=9544;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=21383618; PubMed=11491535; DOI=10.1007/s002510100322;
 RA Villinger F., Bostik P., Wayne A.E., King C.L., Genain C.P.,
 RA Weiss W.R., Ansari A.A.;
 RT "Cloning, sequencing, and homology analysis of nonhuman primate
 RT Fas/Fas-ligand and co-stimulatory molecules.";
 RL Immunogenetics 53:315-328(2001).
 DR EMBL; AF344846; AAK37605.1; -, mRNA.
 DR HSSP; P16410; 1I85.
 DR SMR; Q9BDC4; 37-161.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0006955; P:immune response; IEA.
 DR InterPro; IPR008096; CTLA4.
 DR InterPro; IPR003599; Ig v.
 DR PRINTS; PR01720; CTLANTIGEN4.
 DR SMART; SM00406; IGv; 1.
 KW Signal.
 FT SIGNAL 1 37 Potential.
 SQ SEQUENCE 223 AA; 24683 MW; BDE42248A00398FA CRC64;
 Query Match 11.2%; Score 119; DB 2; Length 223;
 Best Local Similarity 26.7%; Pred. No. 0.044;

Matches	54;	Conservative	25;	Mismatches	95;	Indels	28;	Gaps	6;
Qy	3	WMLLLILIMVHPGSCALWVSQPEIRTLGSSAPLPCSFNASQGRLAIGSVTWFRDEVVP	62						
Db	22	YTLFLSLLFIPIVFSKAMHVAQPAVVLANSRGIASFVCEY-ASPGKATEVRVTVLRQADSQ	80						
Qy	63	GKEVRNGTPEFRGRGLAPLASSRFLHD-----HQAELHIRDVGRGHDAIYVCRVEVL	113						
Db	81	VTEVCAATYMMGNELT-----FLDDSICTGTSSGNQVNLTIQGLRAMDTGLICKVELM	134						
Qy	114	---GLGVGTNGTRLVVEKEHPQLGAGTVLLRA----GFYAVSFLSVAVGSTVYQKGC	166						
Db	135	YPPPYWYGIGNGIQIYVIDPEPCPDSDFLLWILAAVSSGLFFYSFLLTAVSL-----KM	189						
Qy	167	LTKGPRRQLPAVVPAPLPPPC	188						
Db	190	LKKRSPLTTGVYVKMPTEPEC	211						

Search completed: February 27, 2006, 18:03:03
Job time : 233 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 27, 2006, 18:03:18 ; Search time 47 Seconds
(without alignments)
353.570 Million cell updates/sec

Title: US-10-696-259-6

Perfect score: 1067

Sequence: 1 MAMLLILLIMVHPCALW.....APLPCCGSSAHLPLPPVGG 201

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: /cgn2_6/ptodata/1/iaa/5-COMB.pep.*
- 2: /cgn2_6/ptodata/1/iaa/6-COMB.pep.*
- 3: /cgn2_6/ptodata/1/iaa/H-COMB.pep.*
- 4: /cgn2_6/ptodata/1/iaa/PCITUS-COMB.pep.*
- 5: /cgn2_6/ptodata/1/iaa/RE-COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	118.5	11.1	223	2	US-08-228-208A-17
2	118.5	11.1	223	2	US-09-454-651B-17
3	118.5	11.1	223	2	US-09-949-016-11449
4	117	10.9	223	2	US-09-957-688C-1
5	116.5	10.9	223	2	US-09-949-016-6602
6	116.5	10.9	223	2	US-09-957-688C-2
7	116	10.9	226	2	US-09-311-784A-32
8	116	10.9	232	2	US-09-949-016-7589
9	116	10.9	232	2	US-09-949-016-7590
10	115	10.8	223	2	US-09-646-561-42
11	112	10.5	223	2	US-09-646-561-47
12	110	10.3	187	1	US-08-067-684-14
13	110	10.3	187	1	US-08-008-898-14
14	110	10.3	187	1	US-08-459-818-14
15	110	10.3	187	1	US-08-889-666-14
16	110	10.3	187	1	US-08-465-078-14
17	110	10.3	187	1	US-08-725-776-14
18	110	10.3	187	1	US-08-488-062-14
19	110	10.3	187	2	US-08-228-208A-14
20	110	10.3	187	2	US-08-253-783-36
21	110	10.3	187	2	US-09-454-651B-14
22	110	10.3	187	4	PCT-US95-06726-36
23	109	10.2	223	2	US-09-303-040-10
24	106.5	10.0	364	2	US-09-472-087-100
25	106	9.9	223	2	US-09-454-651B-18
26	106	9.9	270	2	US-09-082-593-10
27	105.5	9.9	236	2	US-09-049-672A-7

28	104.5	9.8	238	2	US-09-227-595-30	Sequence 30, Appl
29	104.5	9.8	238	2	US-09-227-595-32	Sequence 32, Appl
30	104.5	9.8	238	2	US-08-595-590B-30	Sequence 30, Appl
31	104.5	9.8	238	2	US-08-595-590B-32	Sequence 32, Appl
32	104	9.7	174	2	US-08-804-180C-4	Sequence 4, Appli
33	103.5	9.7	329	2	US-10-104-047-3709	Sequence 3709, Ap
34	103	9.7	267	1	US-08-416-336-2	Sequence 2, Appli
35	102.5	9.6	152	2	US-09-471-276-855	Sequence 855, App
36	102	9.6	223	2	US-08-228-208A-18	Sequence 18, Appl
37	102	9.6	239	2	US-09-828-995B-26	Sequence 26, Appl
38	102	9.6	377	2	US-09-227-595-24	Sequence 24, Appl
39	102	9.6	377	2	US-08-595-590B-24	Sequence 24, Appl
40	101.5	9.5	374	2	US-09-227-595-26	Sequence 26, Appl
41	101.5	9.5	374	2	US-09-227-595-28	Sequence 28, Appl
42	101.5	9.5	374	2	US-08-595-590B-26	Sequence 26, Appl
43	101.5	9.5	374	2	US-08-595-590B-28	Sequence 28, Appl
44	101	9.5	234	1	US-08-505-058-1	Sequence 1, Appli
45	101	9.5	234	1	US-08-459-818-21	Sequence 21, Appl

ALIGNMENTS

RESULT 1
US-08-228-208A-17
; Sequence 17, Application US/08228208A
; Patent No. 6090914
; GENERAL INFORMATION:
; APPLICANT: Linsley, Peter S.
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Damle, Nitin K.
; APPLICANT: Brady, William
; APPLICANT: Wallace, Philip M.
; TITLE OF INVENTION: CTLA4/CD28Ig HYBRID FUSION
; TITLE OF INVENTION: PROTEINS AND USES THEREOF
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould
; STREET: 11150 Santa Monica Boulevard, Suite 400
; CITY: Los Angeles
; STATE: CA
; COUNTRY: USA
; ZIP: 90025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/228,208A
; FILING DATE: 15-APR-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/008,898
; FILING DATE: 22-JAN-1993
; APPLICATION NUMBER: 07/723,617
; FILING DATE: 27-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Adriano, Sarah B
; REGISTRATION NUMBER: 34,470
; REFERENCE/DOCKET NUMBER: 30436-30US01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 310 445-1140
; TELEFAX: 310 445-9031
; TELEX:
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 223 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-228-208A-17

Query Match 11.1%; Score 118.5; DB 2; Length 223;
Best Local Similarity 27.0%; Pred. No. 0.00037;
Matches 54; Conservative 24; Mismatches 93; Indels 29; Gaps 7;
QY 6 LLILIMVHPCSC-ALMVSQPPETRTLEGSSAFPLPCSNASQGLAIGSVTWFRDEVVPGK 64
DB 24 LLFFLLFIPVFCAMHVAQPAVVLASSRGIAFVCEY-ASPGKATEVRVTVLROADSQVT 82
QY 65 EVRNGTPEFRGRAPLASSRFLHD-----HQAELHIRDVRGHDAIYVCRVEVL-- 113
DB 83 EVCAATYMGNELT-----FLDSDICTGSSGNQVNLTIQGLRAMDTGLYICKVELMYP 136
QY 114 -GLGVGTGNGTRLVVEKEHPQLGAGTVLLRA-----GFYAVSFSLVAVGSTVYVQKCLT 168
DB 137 PPYVLGNGTQIYVIDPEPCDSDFLWLILAAVSSGLFFYSFLLTAVSL- ----KMLK 191
QY 169 WKGPRRQLPAVVPAPLPPPC 188
DB 192 KRSPLTTGVYVYKMPPEPEC 211

RESULT 2
US-09-454-651B-17
; Sequence 17, Application US/09454651B
; Patent No. 6887471
; GENERAL INFORMATION:
; APPLICANT: Linsley, Peter S.
; Ledbetter, Jeffrey A.
; Damle, Nitin K.
; Brady, William
; Wallace, Philip M.
; TITLE OF INVENTION: CTLA4/CD28lg HYBRID FUSION
; PROTEINS AND USES THEREOF
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Mandel & Adriano
; STREET: 35 N. Arroyo Parkway, Suite 60
; CITY: Pasadena
; STATE: California
; COUNTRY: USA
; ZIP: 91103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/454,651B
; FILING DATE: 06-Dec-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/228,208
; FILING DATE: 15-Apr-1994
; APPLICATION NUMBER: 08/008,898
; FILING DATE: 22-JAN-1993
; APPLICATION NUMBER: 07/723,617
; FILING DATE: 27-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Adriano, Sarah B
; REGISTRATION NUMBER: 34,470
; REFERENCE/DOCKET NUMBER: 30436.30USD1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 626 395-7801
; TELEFAX: 626 395-0694
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 223 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: linear
; MOLECULE TYPE: protein

; SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-09-454-651B-17
Query Match 11.1%; Score 118.5; DB 2; Length 223;
Best Local Similarity 27.0%; Pred. No. 0.00037;
Matches 54; Conservative 24; Mismatches 93; Indels 29; Gaps 7;
QY 6 LLILIMVHPCSC-ALMVSQPPETRTLEGSSAFPLPCSNASQGLAIGSVTWFRDEVVPGK 64
DB 24 LLFFLLFIPVFCAMHVAQPAVVLASSRGIAFVCEY-ASPGKATEVRVTVLROADSQVT 82
QY 65 EVRNGTPEFRGRAPLASSRFLHD-----HQAELHIRDVRGHDAIYVCRVEVL-- 113
DB 83 EVCAATYMGNELT-----FLDSDICTGSSGNQVNLTIQGLRAMDTGLYICKVELMYP 136
QY 114 -GLGVGTGNGTRLVVEKEHPQLGAGTVLLRA-----GFYAVSFSLVAVGSTVYVQKCLT 168
DB 137 PPYVLGNGTQIYVIDPEPCDSDFLWLILAAVSSGLFFYSFLLTAVSL- ----KMLK 191
QY 169 WKGPRRQLPAVVPAPLPPPC 188
DB 192 KRSPLTTGVYVYKMPPEPEC 211

RESULT 3
US-09-949-016-11449
; Sequence 11449, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11449
; LENGTH: 232
; TYPE: PRT
; ORGANISM: Human
; US-09-949-016-11449

Query Match 11.1%; Score 118.5; DB 2; Length 232;
Best Local Similarity 27.0%; Pred. No. 0.00039;
Matches 54; Conservative 24; Mismatches 93; Indels 29; Gaps 7;
QY 6 LLILIMVHPCSC-ALMVSQPPETRTLEGSSAFPLPCSNASQGLAIGSVTWFRDEVVPGK 64
DB 33 LLFFLLFIPVFCAMHVAQPAVVLASSRGIAFVCEY-ASPGKATEVRVTVLROADSQVT 91
QY 65 EVRNGTPEFRGRAPLASSRFLHD-----HQAELHIRDVRGHDAIYVCRVEVL-- 113
DB 92 EVCAATYMGNELT-----FLDSDICTGSSGNQVNLTIQGLRAMDTGLYICKVELMYP 145
QY 114 -GLGVGTGNGTRLVVEKEHPQLGAGTVLLRA-----GFYAVSFSLVAVGSTVYVQKCLT 168
DB 146 PPYVLGNGTQIYVIDPEPCDSDFLWLILAAVSSGLFFYSFLLTAVSL- ----KMLK 200
QY 169 WKGPRRQLPAVVPAPLPPPC 188
DB 201 KRSPLTTGVYVYKMPPEPEC 220

RESULT 4
US-09-957-688C-1
; Sequence 1, Application US/09957688C

; Patent No. 6875904
; GENERAL INFORMATION:
; APPLICANT: LIU, YANG
; APPLICANT: ZHENG, PAN
; APPLICANT: LU, PING
; APPLICANT: MOSINGER, BEDRICH
; APPLICANT: MAY, KEN
; TITLE OF INVENTION: ANIMAL MODEL FOR IDENTIFYING AGENTS THAT INHIBIT OR ENHANCE
; FILE REFERENCE: CTIA4 SIGNALING
; CURRENT APPLICATION NUMBER: US/09/957,688C
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 60/234,089
; PRIOR FILING DATE: 2000-09-20
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 223
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-957-688C-1

Query Match 11.0%; Score 117; DB 2; Length 223;
Best Local Similarity 26.1%; Pred. No. 0.00053;
Matches 52; Conservative 28; Mismatches 97; Indels 22; Gaps 7;

Qy 3 WMLLLILMVHPGSCALWVSQPPPEIRTLGSSAFPCSFNASQGRLAIGSVTWFDRD--- 58
Db 22 FVALLTLFIPVFSEALQVTPSVVLASSHGVSFPCEYSPSHNTDEV-RVTVLQTNQD 80
Qy 59 --EVPQKEVNGTPEFRGRAPLASSRFLHDHQAELHIRDVRGHDASIVYCRVEVL--- 113
Db 81 MTEVCATTTEKNTVGFLD--YPCSGTF-NESRVNLTIQGLRAVDGLYLCKVELMYP 137
Qy 114 GLGVGTGNGTRLVVEKEHPQLGAGTVL---LLRAGFVAVSFLSVAVGSIYVYQKCLTW 169
Db 138 PYFVGNGGTQIYVIDPECPDSDFLWLILVAVSLGLFFYSFLVTAVSLS-----KMLK 192
Qy 170 KGRPRQLPAVVPAPLPPPC 188
Db 193 RSPLTGTVYVVKMPTEPEC 211

RESULT 5
US-09-949-016-6602
; Sequence 6602, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6602
; LENGTH: 223
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6602

Query Match 10.9%; Score 116.5; DB 2; Length 223;
Best Local Similarity 27.0%; Pred. No. 0.0006;
Matches 54; Conservative 24; Mismatches 93; Indels 29; Gaps 7;

Qy 6 LLILIMVHPGSC-ALWVSQPPPEIRTLGSSAFPCSFNASQGRLAIGSVTWFDRDVEVP 64

Db 24 LLFFLLFIPVFCCKAMHVAQPAVVVLASSRGIAISFVCEY-ASPGKATEVRVTVLROADSQVT 82
Qy 65 EVRNGTPEFRGRAPLASSRFLHD-----HQAELHIRDVRGHDASIVYCRVEVL-- 113
Db 83 EVCAATYMTGNELT-----FLDSDICTGTSSGNQVNLTIQGLRAMDTGLYICKVELMYP 136
Qy 114 -GLGVGTGNGTRLVVEKEHPQLGAGTVLLRA---GFYAVSFLSVAVGSIYVYQKCLT 168
Db 137 PYYLGTGNGTQIYVIDPECPDSDFLWLILAAVSSGLFFYSFLTAVSLS-----KMLK 191
Qy 169 WKGRPRQLPAVVPAPLPPPC 188
Db 192 KRSPLTTGTVYVVKMPTEPEC 211

RESULT 6
US-09-957-688C-2
; Sequence 2, Application US/09957688C
; Patent No. 6875904
; GENERAL INFORMATION:
; APPLICANT: LIU, YANG
; APPLICANT: ZHENG, PAN
; APPLICANT: LU, PING
; APPLICANT: MOSINGER, BEDRICH
; APPLICANT: MAY, KEN
; TITLE OF INVENTION: ANIMAL MODEL FOR IDENTIFYING AGENTS THAT INHIBIT OR ENHANCE
; TITLE OF INVENTION: CTIA4 SIGNALING
; CURRENT APPLICATION NUMBER: US/09/957,688C
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 60/234,089
; PRIOR FILING DATE: 2000-09-20
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 223
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-957-688C-2

Query Match 10.9%; Score 116.5; DB 2; Length 223;
Best Local Similarity 27.0%; Pred. No. 0.0006;
Matches 54; Conservative 24; Mismatches 93; Indels 29; Gaps 7;

Qy 6 LLILIMVHPGSC-ALWVSQPPPEIRTLGSSAFPCSFNASQGRLAIGSVTWFDRDVEVP 64
Db 24 LLFFLLFIPVFCCKAMHVAQPAVVVLASSRGIAISFVCEY-ASPGKATEVRVTVLROADSQVT 82
Qy 65 EVRNGTPEFRGRAPLASSRFLHD-----HQAELHIRDVRGHDASIVYCRVEVL-- 113
Db 83 EVCAATYMTGNELT-----FLDSDICTGTSSGNQVNLTIQGLRAMDTGLYICKVELMYP 136
Qy 114 -GLGVGTGNGTRLVVEKEHPQLGAGTVLLRA---GFYAVSFLSVAVGSIYVYQKCLT 168
Db 137 PYYLGTGNGTQIYVIDPECPDSDFLWLILAAVSSGLFFYSFLTAVSLS-----KMLK 191
Qy 169 WKGRPRQLPAVVPAPLPPPC 188
Db 192 KRSPLTTGTVYVVKMPTEPEC 211

RESULT 7
US-09-311-784A-32
; Sequence 32, Application US/09311784A
; Patent No. 6534482
; GENERAL INFORMATION:
; APPLICANT: Fikes, John D.
; APPLICANT: Hermanson, Gary G.
; APPLICANT: Sette, Alessandro
; APPLICANT: Ishioka, Glenn Y.
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert W.


```
; PRIOR APPLICATION NUMBER: 09/062,597
; PRIOR FILING DATE: 1998-04-17
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 42
; LENGTH: 223
; TYPE: PRT
; ORGANISM: Canis familiaris
US-09-646-561-42

Query Match          10.8%; Score 115; DB 2; Length 223;
Best Local Similarity 26.6%; Pred. No. 0.00086;
Matches 53; Conservative 24; Mismatches 94; Indels 28; Gaps 6;

Qy 6 LLILIMVHPGSCALWVSPQPIRTLEGSSAFPCSFNASQGLRAIGSVTWFRDVFVPGKE 65
Db 25 LPSLLFIPVFSKGMHVAQPAVVLAASSRGVASFVCEYGSS-GNAAEVRVTVLRQAGSQMTE 83
Qy 66 VRNGTPEPRGRGLAPLASSRFLHD-----HQAEHLIRDVGRGHDASIYVCRVEVL--- 113
Db 84 VCAATYTYVEDELA-----FLDDSTCTGTSSGNKVNLTIOGLRAMDTGLYICKVELMYPP 137
Qy 114 GLGVGTGNGTRLVVEKEHPQLGAGTVLLLR-----GFYAVSFLSVAVGSTVYVQKCLTW 169
Db 138 PYYVGMNGTQIYVIDPEPCDPSDFLLWLAAVSSGLFFYSFLITAVSL-----KMLKK 192
Qy 170 KGRRLQPAVVPAPLPPPC 188
Db 193 RSPLTTGVVVKMPTEPEC 211

RESULT 11
US-09-646-561-47
; Sequence 47, Application US/09646561
; Patent No. 6852847
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Kee
; APPLICANT: Yang, Shumin
; APPLICANT: Sellins, Karen S.
; TITLE OF INVENTION: NOVEL FORMS OF T CELL COSTIMULATORY PROTEINS, NUCLEIC
; FILE REFERENCE: IM-1-Cl-PCT
; CURRENT APPLICATION NUMBER: US/09/646,561
; CURRENT FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: 60/078,765
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 09/062,597
; PRIOR FILING DATE: 1998-04-17
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 47
; LENGTH: 223
; TYPE: PRT
; ORGANISM: Felis catus
US-09-646-561-47

Query Match          10.5%; Score 112; DB 2; Length 223;
Best Local Similarity 26.1%; Pred. No. 0.0017;
Matches 52; Conservative 24; Mismatches 95; Indels 28; Gaps 6;

Qy 6 LLILIMVHPGSCALWVSPQPIRTLEGSSAFPCSFNASQGLRAIGSVTWFRDVFVPGKE 65
Db 25 LPSLLFIPVFSKGMHVAQPAVVLAASSRGVASFVCEYGSS-GNAAEVRVTVLRQAGSQMTE 83
Qy 66 VRNGTPEPRGRGLAPLASSRFLHD-----HQAEHLIRDVGRGHDASIYVCRVEVL--- 113
Db 84 VCAATYTYVENELA-----FLDDSTCTGTSSGNKVNLTIOGLRAMDTGLYICKVELMYPP 137
Qy 114 GLGVGTGNGTRLVVEKEHPQLGAGTVLLLR-----GFYAVSFLSVAVGSTVYVQKCLTW 169
Db 138 PYYAGMNGTQIYVIDPEPCDPSDFLLWLAAVSSGLFFYSFLITAVSL-----KMLKK 192
Qy 170 KGRRLQPAVVPAPLPPPC 188
```

```
Db 193 RSPLTTGVVVKMPTEPEC 211

RESULT 12
US-08-067-684-14
; Sequence 14, Application US/08067684
; Patent No. 5434131
; GENERAL INFORMATION:
; APPLICANT: Linsley, Peter S.
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Damle, Nitin K.
; APPLICANT: Brady, William
; TITLE OF INVENTION: CTLA4 RECEPTOR AND METHODS FOR ITS USE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheldon & Mak
; STREET: 225 South Lake Avenue, Suite 900
; CITY: Pasadena
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 91101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/067,684
; FILING DATE: 26-MAY-1993
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Adriano, Sarah B.
; REGISTRATION NUMBER: 34,470
; REFERENCE/DOCKET NUMBER: 7848-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 310/312-9900
; TELEFAX: 310/479-8340
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 187 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-067-684-14

Query Match          10.3%; Score 110; DB 1; Length 187;
Best Local Similarity 26.7%; Pred. No. 0.0022;
Matches 50; Conservative 22; Mismatches 87; Indels 28; Gaps 6;

Qy 18 ALWVSQPEIRTELEGSSAFPCSFNASQGLRAIGSVTWFRDVFVPGKEVRNGTPEFRGL 77
Db 1 AMHVAQPAVVLAASSRGVASFVCEY-ASPGKATEVRVTVLRQADSQVTEVCAATYMMGNEL 59
Qy 78 APLASSRFLHD-----HQAEHLIRDVGRGHDASIYVCRVEVL---GLGVGTGNGTRL 125
Db 60 T-----FLDDSTCTGTSSGNQVNLTIOGLRAMDTGLYICKVELMYPPYVILGNGTQI 113
Qy 126 VVEKEHPQLGAGTVLLLR-----GFYAVSFLSVAVGSTVYVQKCLTWKGRRLQPAVVP 181
Db 114 YVIDPEPCDPSDFLLWLAAVSSGLFFYSFLITAVSL-----KMLKKRSPLTGTGVVVKM 168
Qy 182 APLPPPC 188
Db 169 PPEPEC 175

RESULT 13
US-08-088-998-14
; Sequence 14, Application US/0808899
; Patent No. 5770197
```


COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/889,666
FILING DATE: 08-JUL-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/375390
FILING DATE: 18-JAN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Adriano, Sarah B.
REGISTRATION NUMBER: 34,470
REFERENCE/DOCKET NUMBER: 30436-35US01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 310-445-1140
TELEFAX: 310-445-9031
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 187 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-889-666-14

Query Match 10.3%; Score 110; DB 1; Length 187;
Best Local Similarity 26.7%; Pred No. 0.0022;
Matches 50; Conservative 22; Mismatches 87; Indels 28; Gaps 6;
Qy 18 ALWVSQPPEIRTLGGSSAFPCSFNASQGRLAIGSVTWFRDEVVFGKEVRNGTPEFRGRL 77
Db 1 AMHVAQPAVAVLASSRGIASFVCEY-ASPGKATEVRVTVLROADSQVTEVCAATYMMGNEL 59
Qy 78 APLASSRFLHD-----HQAELHIRDVRGHDASIYVCRVEVL---GLGVGTGNGTRL 125
Db 60 T-----FLDDSICTGTSSGNQVNLTIQGLRAMDTGLYICKVELMYPYPYLYLGIGNGTQI 113
Qy 126 VVEKEHPQLGAGTVLLRA---GFYAVSFLSVAGSVTYVYQGKCLTWKGP RRQLPAVVP 181
Db 114 YVIDPEPCPSDFLLWILAAVSSGLFFYSFLLTAVSLG-----KMLKRSPLTTGVVYVKM 168
Qy 182 APLPPPC 188
Db 169 PPTPEEC 175

Search completed: February 27, 2006, 18:04:40
Job time : 48 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 27, 2006, 18:04:03 ; Search time 166 Seconds
(without alignments)
505.926 Million cell updates/sec

Title: US-10-696-259-6

Perfect score: 1067

Sequence: 1 MAWLLILIMVHFGSCALW.....APLPPCGSSAHLPPVPGG 201

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA Main.*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1067	100.0	201	4	US-10-696-259-6
2	1017.5	95.4	198	4	US-10-696-259-9
3	876	82.1	190	4	US-10-036-444-2
4	876	82.1	190	6	US-10-696-259-4
5	876	82.1	190	6	US-11-137-649-2
6	859	80.5	177	4	US-10-696-259-5
7	840.5	78.8	185	4	US-10-696-259-7
8	828.5	77.6	161	4	US-10-696-259-10
9	825	77.3	175	4	US-10-696-259-8
10	713	66.8	135	4	US-10-333-481-17
11	713	66.8	369	4	US-10-333-481-18
12	632	59.2	120	4	US-10-036-444-4
13	632	59.2	120	6	US-11-137-649-4
14	125.5	11.8	246	3	US-09-909-567B-49
15	125	11.7	212	3	US-09-898-195A-17
16	125	11.7	212	4	US-10-057-288-12
17	125	11.7	212	4	US-10-155-514-2
18	125	11.7	212	4	US-10-419-008-17
19	125	11.7	212	4	US-10-742-564A-6
20	125	11.7	212	5	US-10-740-645A-6
21	125	11.7	212	5	US-10-910-531-17
22	121.5	11.4	232	4	US-10-225-108A-12
23	121.5	11.4	232	4	US-10-461-148-6
24	118.5	11.1	139	4	US-10-312-495-6
25	118.5	11.1	223	5	US-10-741-600-894
26	118.5	11.1	223	5	US-10-461-000-17
27	117.5	11.0	223	4	US-10-383-201-20

28	117	11.0	223	6	US-11-052-559-1	Sequence 1, Appl
29	116.5	10.9	223	3	US-09-989-545-21	Sequence 21, Appl
30	116.5	10.9	223	3	US-09-928-267-18	Sequence 18, Appl
31	116.5	10.9	223	3	US-09-928-267-21	Sequence 21, Appl
32	116.5	10.9	223	4	US-10-925-519-8	Sequence 8, Appl
33	116.5	10.9	223	4	US-10-207-655-101	Sequence 101, App
34	116.5	10.9	223	5	US-10-688-845-24	Sequence 24, Appl
35	116.5	10.9	223	5	US-10-491-997-76	Sequence 76, Appl
36	116.5	10.9	223	6	US-11-052-559-2	Sequence 2, Appl
37	116.5	10.9	223	6	US-11-120-777-21	Sequence 21, Appl
38	116.5	10.9	382	4	US-10-207-655-316	Sequence 316, App
39	116.5	10.9	382	5	US-10-627-556-86	Sequence 86, Appl
40	116	10.9	226	4	US-10-038-107A-1	Sequence 1, Appl
41	116	10.9	226	4	US-10-371-525-32	Sequence 32, Appl
42	116	10.9	226	4	US-10-371-069-32	Sequence 32, Appl
43	116	10.9	226	4	US-10-371-645-32	Sequence 32, Appl
44	116	10.9	226	4	US-10-371-260-32	Sequence 32, Appl
45	116	10.9	226	4	US-10-411-010-19	Sequence 19, Appl

ALIGNMENTS

RESULT 1
US-10-696-259-6
; Sequence 6, Application US/10696259
; Publication No. US20040110218A1
; GENERAL INFORMATION:
; APPLICANT: BIOGEN INC
; APPLICANT: BROWNING, Jeffrey
; TITLE OF INVENTION: BMOG, A Novel Protein Member of the
; TITLE OF INVENTION: Myelin-Oligodendrocyte Glycoprotein Family and Its Use for
; TITLE OF INVENTION: Immunomodulatory Purposes
; FILE REFERENCE: A041 US
; CURRENT APPLICATION NUMBER: US/10/696,259
; CURRENT FILING DATE: 2003-10-28
; PRIOR APPLICATION NUMBER: US/09/560,855A
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: PCT/US98/23826
; PRIOR FILING DATE: 1998-11-05
; PRIOR APPLICATION NUMBER: 60/064761
; PRIOR FILING DATE: 1997-11-07
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 201
; TYPE: PRT
; ORGANISM: Homo sapien
; US-10-696-259-6

Query Match 100.0%; Score 1067; DB 4; Length 201;
Best Local Similarity 100.0%; Pred. No. 2.7e-91;
Matches 201; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MAWLLILIMVHFGSCALWVSPPEIRTLGSSAFPLPCSFNASQGRLAIGSVTWFRDEV	60
Db	1	MAWLLILIMVHFGSCALWVSPPEIRTLGSSAFPLPCSFNASQGRLAIGSVTWFRDEV	60
Qy	61	VPKKEVRNGTPFERGLAPLASSRFLHDHQAELHIRDVRGHDAIYVCRVEVLGLGVGTG	120
Db	61	VPKKEVRNGTPFERGLAPLASSRFLHDHQAELHIRDVRGHDAIYVCRVEVLGLGVGTG	120
Qy	121	NGTRLVVEKEHPQLGAGTVLLLRAGFYAVSFLSVAGSTVYQCKLITWKGRPQLPAVV	180
Db	121	NGTRLVVEKEHPQLGAGTVLLLRAGFYAVSFLSVAGSTVYQCKLITWKGRPQLPAVV	180
Qy	181	PAPLPPPCGSSAHLPPVPGG	201
Db	181	PAPLPPPCGSSAHLPPVPGG	201

RESULT 2
US-10-696-259-9

```

; Sequence 9, Application US/10696259
; Publication No. US20040110218A1
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC
; APPLICANT: BROWNING, Jeffrey
; TITLE OF INVENTION: BMOG, A Novel Protein Member of the
; TITLE OF INVENTION: Myelin-Oligodendrocyte Glycoprotein Family and Its Use for
; TITLE OF INVENTION: Immunomodulatory Purposes
; FILE REFERENCE: A041 US
; CURRENT APPLICATION NUMBER: US/10/696,259
; CURRENT FILING DATE: 2003-10-28
; PRIOR APPLICATION NUMBER: US/09/560,855A
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: PCT/US98/23826
; PRIOR FILING DATE: 1998-11-05
; PRIOR APPLICATION NUMBER: 60/064761
; PRIOR FILING DATE: 1997-11-07
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 198
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-696-259-9

```

```

Query Match      95.4%; Score 1017.5; DB 4; Length 198;
Best Local Similarity 98.0%; Pred. No. 1.1e-86;
Matches 197; Conservative 0; Mismatches 1; Indels 3; Gaps 3;

QY 1 MAWMLLLILIMVHPGSCALWVSQPPERTLTGSSAFPLPCSFNASQGRLAIGSVTWRDEV 60
DB 1 MAWMLLLILIMVHPGSCALWVSQPPERTLTGSSAFPLPCSFNASQGRLAIGSVTWRDEV 59
QY 61 VPGKEVRNGTPEFRGRAPLASSRFLHDHQAELHIRDVRGHDASIYVCRVEVLGLGVGTG 120
DB 60 VPGKEVRNGTPEFRGRAPLASSRFLHDHQAELHIRDVRGHDASIYVCRVEVLGLGVGTG 118
QY 121 NGTRLVVEKEHPOLGAGTVLLLRAGFYAVSFSLVAVGSTVYYQKCLTWKGP 180
DB 119 NGTRLVVEKEHPOLGAGTVLLLRAGFYAVSFSLVAVGSTVYYHGKCLTWKGP 177
QY 181 PAPLPPPCGSAHLLPPVPGG 201
DB 178 PAPLPPPCGSAHLLPPVPGG 198

```

```

RESULT 3
US-10-036-444-2
; Sequence 2, Application US/10036444
; Publication No. US20020142445A1
; GENERAL INFORMATION:
; APPLICANT: INNATE PHARMA S.A.S.
; APPLICANT: UNIVERSITA DI GENOVA
; TITLE OF INVENTION: "US20020142445A1el triggering receptor involved in natural
; TITLE OF INVENTION: cytotoxicity mediated by human Natural Killer cells and
; TITLE OF INVENTION: antibodies that identify the same"
; FILE REFERENCE: SEQ-FR-1060
; CURRENT APPLICATION NUMBER: US/10/036,444
; CURRENT FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: 09/440,514
; PRIOR FILING DATE: 1999-11-15
; PRIOR APPLICATION NUMBER: 09/456,199
; PRIOR FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 2
; LENGTH: 190
; TYPE: PRT
; ORGANISM: Human NK cell
US-10-036-444-2

```

```

Query Match      82.1%; Score 876; DB 4; Length 190;
Best Local Similarity 89.2%; Pred. No. 1.7e-73;

```

```

Matches 173; Conservative 2; Mismatches 7; Indels 12; Gaps 2;

QY 1 MAWMLLLILIMVHPGSCALWVSQPPERTLTGSSAFPLPCSFNASQGRLAIGSVTWRDEV 60
DB 1 MAWMLLLILIMVHPGSCALWVSQPPERTLTGSSAFPLPCSFNASQGRLAIGSVTWRDEV 60
QY 61 VPGKEVRNGTPEFRGRAPLASSRFLHDHQAELHIRDVRGHDASIYVCRVEVLGLGVGTG 120
DB 61 VPGKEVRNGTPEFRGRAPLASSRFLHDHQAELHIRDVRGHDASIYVCRVEVLGLGVGTG 120
QY 121 NGTRLVVEKEHPOLGAGTVLLLRAGFYAVSFSLVAVGSTVYYQK-----CLTWKGP 172
DB 121 NGTRLVVEKEHPOLGAGTVLLLRAGFYAVSFSLVAVGSTVYYQKCHMGTCHSSDGP 180
QY 173 RRQLPAVVPAPLPP 186
DB 181 R----GVPEPRCP 190

```

```

RESULT 4
US-10-696-259-4
; Sequence 4, Application US/10696259
; Publication No. US20040110218A1
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC
; APPLICANT: BROWNING, Jeffrey
; TITLE OF INVENTION: BMOG, A Novel Protein Member of the
; TITLE OF INVENTION: Myelin-Oligodendrocyte Glycoprotein Family and Its Use for
; TITLE OF INVENTION: Immunomodulatory Purposes
; FILE REFERENCE: A041 US
; CURRENT APPLICATION NUMBER: US/10/696,259
; CURRENT FILING DATE: 2003-10-28
; PRIOR APPLICATION NUMBER: US/09/560,855A
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: PCT/US98/23826
; PRIOR FILING DATE: 1998-11-05
; PRIOR APPLICATION NUMBER: 60/064761
; PRIOR FILING DATE: 1997-11-07
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 190
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-696-259-4

```

```

Query Match      82.1%; Score 876; DB 4; Length 190;
Best Local Similarity 89.2%; Pred. No. 1.7e-73;
Matches 173; Conservative 2; Mismatches 7; Indels 12; Gaps 2;

QY 1 MAWMLLLILIMVHPGSCALWVSQPPERTLTGSSAFPLPCSFNASQGRLAIGSVTWRDEV 60
DB 1 MAWMLLLILIMVHPGSCALWVSQPPERTLTGSSAFPLPCSFNASQGRLAIGSVTWRDEV 60
QY 61 VPGKEVRNGTPEFRGRAPLASSRFLHDHQAELHIRDVRGHDASIYVCRVEVLGLGVGTG 120
DB 61 VPGKEVRNGTPEFRGRAPLASSRFLHDHQAELHIRDVRGHDASIYVCRVEVLGLGVGTG 120
QY 121 NGTRLVVEKEHPOLGAGTVLLLRAGFYAVSFSLVAVGSTVYYQK-----CLTWKGP 172
DB 121 NGTRLVVEKEHPOLGAGTVLLLRAGFYAVSFSLVAVGSTVYYQKCHMGTCHSSDGP 180
QY 173 RRQLPAVVPAPLPP 186
DB 181 R----GVPEPRCP 190

```

```

RESULT 5
US-11-137-649-2
; Sequence 2, Application US/11137649
; Publication No. US20050221438A1
; GENERAL INFORMATION:
; APPLICANT: INNATE PHARMA S.A.S.

```



```

; APPLICANT: UNIVERSITA DI GENOVA
; TITLE OF INVENTION: "Novel triggering receptor involved in natural
; cytotoxicity mediated by human Natural Killer cells and
; antibodies that identify the same"
; FILE REFERENCE: SEQ-PR-1060
; CURRENT APPLICATION NUMBER: US/11/137,649
; PRIOR FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US/10/036,444
; PRIOR FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: 09/440,514
; PRIOR FILING DATE: 1999-11-15
; PRIOR APPLICATION NUMBER: 09/456,199
; PRIOR FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 2
; LENGTH: 190
; TYPE: PRT
; ORGANISM: Human NK cell
; ORGANISM: Homo sapien
US-11-137-649-2

Query Match      82.1%; Score 876; DB 6; Length 190;
Best Local Similarity 89.2%; Pred. No. 1.7e-73;
Matches 173; Conservative 2; Mismatches 7; Indels 12; Gaps 2;

Qy 1 MAMLLILIMVHPGSCALWVSQPPEIRTLTGSSAFPLPCSFNASQGRLAIGSVTWFDEV 60
   |||||
Db 1 MAMLLILIMVHPGSCALWVSQPPEIRTLTGSSAFPLPCSFNASQGRLAIGSVTWFDEV 60
   |||||

Qy 61 VPGKEVRNGTPEFRGLAPLASSRFLDHQAEHLHIRDVGRGHDAIYVCRVEVLGLGVGTG 120
   |||||
Db 61 VPGKEVRNGTPEFRGLAPLASSRFLDHQAEHLHIRDVGRGHDAIYVCRVEVLGLGVGTG 120
   |||||

Qy 121 NGTRLVVEKEHPQLGAGTVLLLRAGFYAVSFLSVAVGSTVYVYQK 165
   |||||
Db 121 NGTRLVVEKEHPQLGAGTVLLLRAGFYAVSFLSVAVGSTVYVYQK 165
   |||||

RESULT 6
US-10-696-259-5
; Sequence 5, Application US/10696259
; Publication No. US20040110218A1
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC
; TITLE OF INVENTION: BMOG, A Novel Protein Member of the
; Myelin-Oligodendrocyte Glycoprotein Family and Its Use for
; Immunomodulatory Purposes
; FILE REFERENCE: A041 US
; CURRENT APPLICATION NUMBER: US/10/696,259
; CURRENT FILING DATE: 2003-10-28
; PRIOR APPLICATION NUMBER: US/09/560,855A
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: PCT/US98/23826
; PRIOR FILING DATE: 1998-11-05
; PRIOR APPLICATION NUMBER: 60/064761
; PRIOR FILING DATE: 1997-11-07
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 177
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-696-259-5

Query Match      80.5%; Score 859; DB 4; Length 177;
Best Local Similarity 100.0%; Pred. No. 6e-72;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

US-10-696-259-5
; Sequence 5, Application US/10696259
; Publication No. US20040110218A1
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC
; TITLE OF INVENTION: BMOG, A Novel Protein Member of the
; Myelin-Oligodendrocyte Glycoprotein Family and Its Use for
; Immunomodulatory Purposes
; FILE REFERENCE: A041 US
; CURRENT APPLICATION NUMBER: US/10/696,259
; CURRENT FILING DATE: 2003-10-28
; PRIOR APPLICATION NUMBER: US/09/560,855A
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: PCT/US98/23826
; PRIOR FILING DATE: 1998-11-05
; PRIOR APPLICATION NUMBER: 60/064761
; PRIOR FILING DATE: 1997-11-07
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 177
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-696-259-5
; Sequence 5, Application US/10696259
; Publication No. US20040110218A1
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC
; TITLE OF INVENTION: BMOG, A Novel Protein Member of the
; Myelin-Oligodendrocyte Glycoprotein Family and Its Use for
; Immunomodulatory Purposes
; FILE REFERENCE: A041 US
; CURRENT APPLICATION NUMBER: US/10/696,259
; CURRENT FILING DATE: 2003-10-28
; PRIOR APPLICATION NUMBER: US/09/560,855A
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: PCT/US98/23826
; PRIOR FILING DATE: 1998-11-05
; PRIOR APPLICATION NUMBER: 60/064761
; PRIOR FILING DATE: 1997-11-07
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-696-259-7

Query Match      78.8%; Score 840.5; DB 4; Length 185;
Best Local Similarity 89.8%; Pred. No. 3.3e-70;
Matches 168; Conservative 1; Mismatches 15; Indels 3; Gaps 3;

Qy 1 MAMLLILIMVHPGSCALWVSQPPEIRTLTGSSAFPLPCSFNASQGRLAIGSVTWFDEV 60
   |||||
Db 1 MAMLLILIMVHPGSCALWVSQPPEIRTLTGSSAFPLPCSFNASQGRLAIGSVTWFDEV 59
   |||||

Qy 61 VPGKEVRNGTPEFRGLAPLASSRFLDHQAEHLHIRDVGRGHDAIYVCRVEVLGLGVGTG 120
   |||||
Db 60 VPGKEVRNGTPEFRGLAPLASSRFLDHQAEHLHIRDVGRGHDAIYVCRVE-LGLGVGTG 118
   |||||

Qy 121 NGTRLVVEKEHPQLGAGTVLLLRAGFYAVSFLSVAVGSTVYVYQKCLTWKGP 179
   |||||
Db 119 NGTRLVVEKEHPQLGAGTVLLLRAGFYAVSFLSVAVGSTVYVYHGKCHCHMGTHCHSDGV 178
   |||||

Qy 180 VPAPLPP 186
   :|||
Db 179 IPEPRCP 185
   :|||

RESULT 8
US-10-696-259-10
; Sequence 10, Application US/10696259
; Publication No. US20040110218A1
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC
; APPLICANT: BROWNING, Jeffrey
; TITLE OF INVENTION: BMOG, A Novel Protein Member of the
; Myelin-Oligodendrocyte Glycoprotein Family and Its Use for
; Immunomodulatory Purposes
; FILE REFERENCE: A041 US
; CURRENT APPLICATION NUMBER: US/10/696,259
```

```

Qy 1 MAMLLILIMVHPGSCALWVSQPPEIRTLTGSSAFPLPCSFNASQGRLAIGSVTWFDEV 60
   |||||
Db 1 MAMLLILIMVHPGSCALWVSQPPEIRTLTGSSAFPLPCSFNASQGRLAIGSVTWFDEV 60
   |||||

Qy 61 VPGKEVRNGTPEFRGLAPLASSRFLDHQAEHLHIRDVGRGHDAIYVCRVEVLGLGVGTG 120
   |||||
Db 61 VPGKEVRNGTPEFRGLAPLASSRFLDHQAEHLHIRDVGRGHDAIYVCRVEVLGLGVGTG 120
   |||||

Qy 121 NGTRLVVEKEHPQLGAGTVLLLRAGFYAVSFLSVAVGSTVYVYQK 165
   |||||
Db 121 NGTRLVVEKEHPQLGAGTVLLLRAGFYAVSFLSVAVGSTVYVYQK 165
   |||||

RESULT 7
US-10-696-259-7
; Sequence 7, Application US/10696259
; Publication No. US20040110218A1
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC
; APPLICANT: BROWNING, Jeffrey
; TITLE OF INVENTION: BMOG, A Novel Protein Member of the
; Myelin-Oligodendrocyte Glycoprotein Family and Its Use for
; Immunomodulatory Purposes
; FILE REFERENCE: A041 US
; CURRENT APPLICATION NUMBER: US/10/696,259
; CURRENT FILING DATE: 2003-10-28
; PRIOR APPLICATION NUMBER: US/09/560,855A
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: PCT/US98/23826
; PRIOR FILING DATE: 1998-11-05
; PRIOR APPLICATION NUMBER: 60/064761
; PRIOR FILING DATE: 1997-11-07
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-696-259-7

Query Match      78.8%; Score 840.5; DB 4; Length 185;
Best Local Similarity 89.8%; Pred. No. 3.3e-70;
Matches 168; Conservative 1; Mismatches 15; Indels 3; Gaps 3;

Qy 1 MAMLLILIMVHPGSCALWVSQPPEIRTLTGSSAFPLPCSFNASQGRLAIGSVTWFDEV 60
   |||||
Db 1 MAMLLILIMVHPGSCALWVSQPPEIRTLTGSSAFPLPCSFNASQGRLAIGSVTWFDEV 59
   |||||

Qy 61 VPGKEVRNGTPEFRGLAPLASSRFLDHQAEHLHIRDVGRGHDAIYVCRVEVLGLGVGTG 120
   |||||
Db 60 VPGKEVRNGTPEFRGLAPLASSRFLDHQAEHLHIRDVGRGHDAIYVCRVE-LGLGVGTG 118
   |||||

Qy 121 NGTRLVVEKEHPQLGAGTVLLLRAGFYAVSFLSVAVGSTVYVYQKCLTWKGP 179
   |||||
Db 119 NGTRLVVEKEHPQLGAGTVLLLRAGFYAVSFLSVAVGSTVYVYHGKCHCHMGTHCHSDGV 178
   |||||

Qy 180 VPAPLPP 186
   :|||
Db 179 IPEPRCP 185
   :|||

RESULT 8
US-10-696-259-10
; Sequence 10, Application US/10696259
; Publication No. US20040110218A1
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC
; APPLICANT: BROWNING, Jeffrey
; TITLE OF INVENTION: BMOG, A Novel Protein Member of the
; Myelin-Oligodendrocyte Glycoprotein Family and Its Use for
; Immunomodulatory Purposes
; FILE REFERENCE: A041 US
; CURRENT APPLICATION NUMBER: US/10/696,259
```



```
; SEQ ID NO 17
; LENGTH: 212
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-898-195A-17

Query Match      11.7%; Score 125; DB 3; Length 212;
Best Local Similarity 27.1%; Pred. No. 0.0023;
Matches 55; Conservative 26; Mismatches 92; Indels 30; Gaps 7;

Qy      4 MLLILIMVHP--GSCALWYSQPPEIRITLEGSSAFPCSFNASQGRLAIGSVTWFRDEVV 61
Db      10 LLSLVALLPSPMASMAHVAQPAVVLASSRGIAFVCEY-ASPGKATEVRVTVLRQADS 68
Qy      62 PGKEVRNGTPEFRGR LAPLASSRFLHD-----HQAELHIRDVRGHDASIYVCREV 112
Db      69 QVTEVCAATYMGNELT-----FLDDSICTGTSSGNQVNLTIQGLRAMDTGLYICKVEL 122
Qy      113 L---GLGVGTGNGTRLVVEKEHPQLGAGTVLLLA-----GFYAVSELSVAVGSTVYYQ GK 165
Db      123 MYPPPYLIGNGTQIYVIDPEPCPSDFLLWILA AVSSGLFFYFSLTAVSL S-----K 177
Qy      166 CLTWKPRRQLPAVVPAPLP PPC 188
Db      178 MLKKSPLTTGVVYKMPPTPEEC 200
```

Search completed: February 27, 2006, 18:07:33
Job time : 167 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 27, 2006, 18:04:53 ; Search time 19 Seconds
(without alignments)
157.491 Million cell updates/sec

Title: US-10-696-259-6
Perfect score: 1067
Sequence: 1 MAWMLLLILIMVHFGSCALW.....APLPPPCSSAHLPPVPGG 201

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 117670 seqs, 14887254 residues

Total number of hits satisfying chosen parameters: 117670

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA_New:*
1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB pep.*
2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB pep.*
3: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB pep.*
4: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB pep.*
5: /cgn2_6/ptodata/1/pubpaa/US03_NEW_PUB pep.*
6: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB pep.*
7: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB pep.*
8: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	118.5	11.1	223	6	US-10-866-120-8
2	115	10.8	223	7	US-11-057-923-4
3	106.5	10.0	364	7	US-11-128-900-100
4	106	9.9	186	7	US-11-057-923-1
5	105	9.8	205	7	US-11-128-440-9
6	103.5	9.7	329	7	US-11-072-512-3709
7	102.5	9.6	252	7	US-11-054-515-1495
8	101.5	9.5	555	6	US-10-821-234-1015
9	98	9.2	240	7	US-11-000-463-248
10	98	9.2	508	7	US-11-072-512-3233
11	96.5	9.0	234	7	US-11-139-499-2
12	95	8.9	253	7	US-11-054-515-1545
13	94.5	8.9	236	7	US-11-000-463-815
14	94.5	8.9	247	7	US-11-062-186-62
15	94.5	8.9	247	7	US-11-033-039-877
16	94.5	8.9	252	7	US-11-062-186-66
17	94	8.8	708	6	US-10-511-538-229
18	93.5	8.8	203	7	US-11-062-186-70
19	93.5	8.8	206	7	US-11-062-186-69
20	93.5	8.8	208	7	US-11-062-186-63
21	93.5	8.8	213	7	US-11-062-186-67
22	93.5	8.8	224	7	US-11-062-186-64
23	93.5	8.8	229	7	US-11-062-186-68
24	92	8.6	215	6	US-10-374-954-7
25	92	8.6	241	5	US-09-978-360A-571

26	92	8.6	248	7	US-11-054-515-2070	Sequence 2070, Ap
27	91.5	8.6	232	7	US-11-000-463-755	Sequence 755, App
28	91	8.5	250	7	US-11-054-515-1484	Sequence 1484, Ap
29	90.5	8.5	628	7	US-11-080-991-108	Sequence 108, App
30	90	8.4	251	7	US-11-054-515-1207	Sequence 1207, Ap
31	89.5	8.4	110	6	US-10-982-440-50	Sequence 50, Appl
32	89.5	8.4	249	7	US-11-054-515-1570	Sequence 1570, Ap
33	89.5	8.4	250	7	US-11-054-515-1563	Sequence 1563, Ap
34	89.5	8.4	250	7	US-11-054-515-1564	Sequence 1564, Ap
35	89.5	8.4	250	7	US-11-054-515-1574	Sequence 1574, Ap
36	89.5	8.4	1700	6	US-10-453-372-398	Sequence 398, App
37	89.5	8.4	1700	6	US-10-453-372-412	Sequence 412, App
38	89.5	8.4	1700	6	US-10-453-372-414	Sequence 414, App
39	89.5	8.4	1700	6	US-10-453-372-416	Sequence 416, App
40	89.5	8.4	1700	6	US-10-453-372-418	Sequence 418, App
41	89	8.3	281	7	US-11-087-177-3	Sequence 3, Appli
42	89	8.3	282	6	US-10-055-877-127	Sequence 127, App
43	89	8.3	282	7	US-11-087-177-9	Sequence 9, Appli
44	89	8.3	304	7	US-11-087-177-4	Sequence 4, Appli
45	89	8.3	305	6	US-10-055-877-126	Sequence 126, App

ALIGNMENTS

RESULT 1
US-10-866-120-8
; Sequence 8, Application US/10866120
; Publication No. US2005027173A1
; GENERAL INFORMATION:
; APPLICANT: Chin, Li-Te
; TITLE OF INVENTION: METHOD FOR PRODUCING HUMAN ANTIBODIES OF AGONIST, ANTAGONIST, OR
; TITLE OF INVENTION: INVERSE AGONIST
; FILE REFERENCE: P7226/0600
; CURRENT APPLICATION NUMBER: US/10/866,120
; CURRENT FILING DATE: 2004-06-14
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 8
; LENGTH: 223
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(223)
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: P16410
; DATABASE ENTRY DATE: 2004-03-15
; RELEVANT RESIDUES: (1)..(223)
US-10-866-120-8

Query Match	11.1%	Score 118.5;	DB 6;	Length 223;
Best Local Similarity	27.0%;	Pred. No. 0.00057;		
Matches	54;	Conservative	24;	Mismatches 93;
				Indels 29;
				Gaps 7;
Oy	6	LLIILIMVHFGSC-ALWVSQPPEIRTELEGSSAFPCSFNAGSLAIGSVTWFRDEWVPGK	64	
Db	24	LLFELLIPVFCCKAHVQAQPAVVLASSRGATSFCEY-ASPCKATEVTVTLROADSQVT	82	
Oy	65	EVRNGTPEFRGLAPLASSRFLHD-----HQAELHIRDVGRHDASIYVCRVEVL--	113	
Db	83	EVCAATYMGNELT-----FLDDSICTGTSSGNQVNLTIQGLRAMDTGLYICKVELMYP	136	
Oy	114	-GLGVGTGNGTRLVVEKEHPOLGAGTVLLRA----GEYAVSFILSVAGSVTVYQGKCLT	168	
Db	137	PPYILGNGTQIYVIDPEPCPDSDFLLWLILAAVSSGLFFYSFLTAVLSL-----KMLK	191	
Oy	169	WKGPRRQLPAVVPAPLPPPC	188	
Db	192	KRSLTTGTGVYKMPTEPEC	211	

```
RESULT 2
US-11-057-923-4
; Sequence 4, Application US/11057923
; Publication No. US20050287152A1
; GENERAL INFORMATION:
; APPLICANT: AMGEN INC.
; APPLICANT: Khare, Sanjay D.
; APPLICANT: Feige, Ulrich
; TITLE OF INVENTION: COMPOSITIONS AND METHODS TO MODULATE AN IMMUNE RESPONSE TO AN
; TITLE OF INVENTION: IMMUNOGENIC THERAPEUTIC AGENT
; FILE REFERENCE: 54113.8008.WO00
; CURRENT APPLICATION NUMBER: US/11/057,923
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: PCT/US04/35415
; PRIOR FILING DATE: 2004-10-26
; PRIOR APPLICATION NUMBER: US 60/515,199
; PRIOR FILING DATE: 2003-10-27
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4
; LENGTH: 223
; TYPE: PRT
; ORGANISM: Mus musculus
; NAME/KEY: MISC FEATURE
; OTHER INFORMATION: Murine CTLA-4
US-11-057-923-4
Query Match 10.8%; Score 115; DB 7; Length 223;
Best Local Similarity 26.1%; Pred. No. 0.0012;
Matches 52; Conservative 28; Mismatches 97; Indels 22; Gaps 7;
QY 3 WMLLLILIMVHGPSCALWVSQPPPIRTLEGSSAFPCSFNASQGRLAIGSVTWFRD--- 58
DB 22 FVALLTLFLIFVFESEAQTQPSVVVLASSHGVSFPCEPSPSHTNDEV-RVTVLRTNDQ 80
QY 59 --EVVPGKEVRNGTPPEGRGLAPLASSRFLHDHQAELHIRDVGRGHDAIYVCRVEVL--- 113
DB 81 MTEVCATFTTEKNTVGFD--YPCSGTF--NESRVNLTIOGLRAVDGTGLYCKVELMYPP 137
QY 114 GLGVGTGNGTRLVVEKEHPQLGAGTVL---LLRAGFYAVSFLSVAGSTVYVQKCLTW 169
DB 138 PYFVGMGNGTQIVIDPEPCDPSDFLLWILVAVSLGLFFYSFLVSAVSL---KMLKK 192
QY 170 KGPRQLPAVVPALPPPC 188
DB 193 RSLPTTGVYVVKMPTEPEC 211
RESULT 3
US-11-128-900-100
; Sequence 100, Application US/11128900
; Publication No. US20050287136A1
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, EILEEN B.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEORFREY
; APPLICANT: CORVALAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PFI DIV3
; CURRENT APPLICATION NUMBER: US/11/128,900
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: US 10/776649
; PRIOR FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: US 10/612497
; PRIOR APPLICATION NUMBER: 2003-07-01
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: US 60/113647
; PRIOR FILING DATE: 1998-12-23
```

```
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 100
; LENGTH: 364
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-128-900-100
Query Match 10.0%; Score 106.5; DB 7; Length 364;
Best Local Similarity 28.0%; Pred. No. 0.013;
Matches 40; Conservative 20; Mismatches 62; Indels 21; Gaps 5;
QY 4 MLLLLILIMVHP--GSCALWVSQPPPIRTLEGSSAFPCSFNASQGRLAIGSVTWFRDEV 61
DB 10 LLSLVLLALFPMSAMAMHVAQPAVVLASSRGIAFVCEY-ASPGKATEVRVIVLRQADS 68
QY 62 PGKEVRNGTPPEGRGLAPLASSRFLHD-----HQAELHIRDVGRGHDAIYVCRVEV 112
DB 69 QVTEVCAATYMMGNELT-----FLDDSICTGTSSGNQVNLTIQGLRAMDTGLYCKVEL 122
QY 113 L---GLGVGTGNGTRLVVEKEHP 132
DB 123 MYPPPYLIGIGNGTQIYVIDPEP 145
RESULT 4
US-11-057-923-1
; Sequence 1, Application US/11057923
; Publication No. US20050287152A1
; GENERAL INFORMATION:
; APPLICANT: AMGEN INC.
; APPLICANT: Khare, Sanjay D.
; APPLICANT: Feige, Ulrich
; TITLE OF INVENTION: COMPOSITIONS AND METHODS TO MODULATE AN IMMUNE RESPONSE TO AN
; TITLE OF INVENTION: IMMUNOGENIC THERAPEUTIC AGENT
; FILE REFERENCE: 54113.8008.WO00
; CURRENT APPLICATION NUMBER: US/11/057,923
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: PCT/US04/35415
; PRIOR FILING DATE: 2004-10-26
; PRIOR APPLICATION NUMBER: US 60/515,199
; PRIOR FILING DATE: 2003-10-27
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1
; LENGTH: 186
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: MISC FEATURE
; OTHER INFORMATION: Full-length human CTLA-4 amino acid sequence
US-11-057-923-1
Query Match 9.9%; Score 106; DB 7; Length 186;
Best Local Similarity 26.6%; Pred. No. 0.0066;
Matches 49; Conservative 21; Mismatches 86; Indels 28; Gaps 6;
QY 21 VSQPPPIRTLEGSSAFPCSFNASQGRLAIGSVTWFRDEVVPGKEVRNGTPPEGRGLAPL 80
DB 3 VAQPAVVLASSRGIAFVCEY-ASPGKATEVRVTVLRQADSQVTEVCAATYMMGNELT-- 59
QY 81 ASSRFLHD-----HQAELHIRDVGRGHDAIYVCRVEVL---GLGVGTGNGTRLVVE 128
DB 60 ----FLDDSICTGTSSGNQVNLTIQGLRAMDTGLYCKVELMYPYVIGIGNGTQIYVI 115
QY 129 KEHPQLGAGTVLLRA-----GFYAVSFLSVAGSTVYVQKCLTWKGPRLQPAVVPAPL 184
DB 116 DPEPCDPSDFLLWILAAVSSGLFFYSFLTAVSL-----KMLKRSPLTTGVYVVKMPPT 170
QY 185 PPC 188
DB 171 EPEC 174
```

```
RESULT 5
US-11-128-440-9
; Sequence 9, Application US/11128440
; Publication No. US20050261478A1
; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Hayden-Ledbetter, Martha
; APPLICANT: Brady, William A.
; APPLICANT: Grosmaitre, Laura S.
; APPLICANT: Law, Che-Leung
; APPLICANT: Dua, Raj
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR REGULATING
; TITLE OF INVENTION: LYMPHOCTE ACTIVATION
; FILE REFERENCE: 980034.408D1
; CURRENT APPLICATION NUMBER: US/11/128,440
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: US 10/646,381
; PRIOR FILING DATE: 2003-08-21
; PRIOR APPLICATION NUMBER: US 09/252,150
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/108,683
; PRIOR FILING DATE: 1998-11-16
; PRIOR APPLICATION NUMBER: 60/075,274
; PRIOR FILING DATE: 1998-02-19
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 205
; TYPE: PRT
; ORGANISM: Llama llama
US-11-128-440-9
```

```
Query Match          9.8%; Score 105; DB 7; Length 205;
Best Local Similarity 24.9%; Pred. No. 0.0091;
Matches 50; Conservative 15; Mismatches 56; Indels 80; Gaps 12;

Qy 32 GSSAFPCSFNASQGR-----LAIGSVTFRDEVPVGVKVRNGTPEFRGRRLAPLASSRFLH 87
    |||||
Db 15 GDSLRLLSC--AASGRFTFTYAMG--WFRQ--APGKE-----PEFVARISRVSSTFYT 61
    |||||

Qy 88 D-----HQAELHIRDVRGHDASIYCRVEVLGLVGTGNGTRLVVEKEHPQ 133
    |||||
Db 62 DSVKGRFTISRDNAKNTMYLQNMGMKAEDTAVYYCAAD-----SDYGPGR--SSEYDY 113

Qy 134 LGAGTVLLLRAGFAVSFLSVAGSVTVYQKCLTWKGRQLPAVVPAPLPP--C 188
    |||||
Db 114 WQGT-----QTVSSE-----PKTPKPOPOPOPNPTTSKC 147

Qy 189 -----GSSAHLPPVP 199
    |||||
Db 148 PKRPAPELLGSPSVFPPKP 168
```

```
RESULT 6
US-11-072-512-3709
; Sequence 3709, Application US/11072512
; Publication No. US20060029945A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOCHIKO
```

```
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: 084335-0191
; CURRENT APPLICATION NUMBER: US/11/072,512
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: US 60/350,978
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: JP 2001-379298
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3709
; LENGTH: 329
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-072-512-3709

Query Match          9.7%; Score 103.5; DB 7; Length 329;
Best Local Similarity 27.9%; Pred. No. 0.022;
Matches 29; Conservative 11; Mismatches 37; Indels 27; Gaps 3;

Qy 15 GSCALWVSQP-----PEIRTEGSAFLPCSFNASQGRLAIGSVTFRDEVPVGVKVR 67
    |||||
Db 159 GKTRLVVQVPVVIENGLPDLSTTEGSHAFLPCKARGSP-----PNITWDKD----- 205
    |||||

Qy 68 NCTPEFRGLAPLASSRFLHQAELHIRDVRGHDASIYCRVE 111
    |||||
Db 206 -----GQPVSGAEGKFTIQPSGELLVKNLEGODAGTYTCTAE 242
    |||||
```

```
RESULT 7
US-11-054-515-1495
; Sequence 1495, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1495
; LENGTH: 252
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1495

Query Match          9.6%; Score 102.5; DB 7; Length 252;
Best Local Similarity 29.0%; Pred. No. 0.02;
```

Matches 36; Conservative 16; Mismatches 49; Indels 23; Gaps 6;
QY 15 GSCALWVSQPEIRTEGSAFLPCSFNASQGLAIGSVTWFRDEVVVGKEVR----- 67
Db 139 GSAQSVVTPPSVAAPGQGVTTSCS--GSSNIGINSVSWYQQ--LPGKAPKLLIYNNS 194
QY 68 --NGTPEPRGRRLAPLASSRFLHDHQAELHIRDVRGHDASIYVCRVEVLGL-GVGTGNGT 123
Db 195 NRFSQVP---GRFSGSKSGT-----SASLAITGLQAEDEADYYCQSYDNSLNGVLFGGCT 246
QY 124 RLTV 127
Db 247 QLTV 250

RESULT 8
US-10-821-234-1015
; Sequence 1015, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: DE SEQ_genes Version 1.0
; SEQ ID NO 1015
; LENGTH: 555
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1015

Query Match 9.5%; Score 101.5; DB 6; Length 555;
Best Local Similarity 25.6%; Pred. No. 0.062; Indels 27; Gaps 5;
Matches 40; Conservative 16; Mismatches 73; Indels 27; Gaps 5;
QY 2 AWMLLILIMVHGPSALWVSQPEIRTEGSAFLPCSFNASQGLAIGSVTWFRDEV 60
Db 59 AWMLLILIMVHGPSALWVSQPEIRTEGSAFLPCSFNASQGLAIGSVTWFRDEV 60
QY 61 VPG-----KEVRNGTPEPRGRLA-----PLASSRFLHDHQAELHIRDVRGHDAS 104
Db 118 GGAQELALLHSKYGLHVSAPYEGRVEQPPPPRNPDLGDSVLL-----RNAVQADEG 168
QY 105 IYVCRVEVLGLGVGTGNGTRLVVEKEHPQLGAGTVL 140
Db 169 EYECRVSTFPAGSFQARLRRLRVLPPLSLNPGPAL 204

RESULT 9
US-11-000-463-248
; Sequence 248, Application US/11000463
; Publication No. US20050266423A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Chen, Rui-hong
; APPLICANT: Qian, Xiaohong B.
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wehrman, Tom
; APPLICANT: Zhang, Jie
; APPLICANT: Zhou, Ping
; APPLICANT: Cao, Yi-Cheng
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
; FILE REFERENCE: 785CIP4CN

; CURRENT APPLICATION NUMBER: US/11/000,463
; CURRENT FILING DATE: 2004-11-29
; PRIOR APPLICATION NUMBER: 10/291,265
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: PCT/US01/02623
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 09/922,279
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/617,746
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 09/631,451
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 09/633,870
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 944
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 248
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-000-463-248
Query Match 9.2%; Score 98; DB 7; Length 240;
Best Local Similarity 25.0%; Pred. No. 0.049;
Matches 54; Conservative 26; Mismatches 76; Indels 60; Gaps 13;
QY 1 MAMMLLLILIMVHGPS---CALWVSQPEIRTEGSSAFPLPCSFNASQGLAIGSV--- 53
Db 6 MAMMLLLILIMVHGPS---CALWVSQPEIRTEGSSAFPLPCSFNASQGLAIGSV--- 53
QY 54 --TWFRDEVVVGKEVRNGTPEPRGRL--APLASSRF---LHDHQAELHIRDVRGHDASIYV 107
Db 58 YPSWHQQ--TPGQPPR--TLIYNTHIRASGVSDRFGSSIVGNKAALTITGAQADDECYYY 113
QY 108 CRVEVLGLGVGT--GNGTRLVV-----EKEHPOLGAGTVLLLRAGFY--AV 149
Db 114 C-VLYMGNDISLFGGGTRLTVLGQPKAAPSVTLFPPSSELSQANKATLVCLISDFYPGAV 172
QY 150 SFLSVAVGSTVYVYGGKCLTWKGRRLPAPVVPAPLP 185
Db 173 T-----VANKADSSPVKAGVETTP 192
RESULT 10
US-11-072-512-3233
; Sequence 3233, Application US/11072512
; Publication No. US20060029945A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: MAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SERI, NAOHICO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOTYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: 084335-0191
; CURRENT APPLICATION NUMBER: US/11/072,512
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: US 60/350,978

Db	7	LLGLLLWLFPCARCAVELTQPPSVSGTARITCGGDNRSNEY-----VHWYQKPKARA	63
Qy	60	-----VWPKKEVRNGTPE-FRGRPLAPLASSRFLHDHQAELHIRDVRGHDAIYVC-----	108
Db	63	PILVIYDDSDRPSGIPERFSGSKS-----GNTATLTINGEAGDADYVCQWWDRA	113
Qy	109	-----RVEVLGLGVGTGNGTRLVWEKEHPQLGAGTGVLLLRAGFY--AVSFSLVAV	156
Db	114	SDHPVFGGGRVTVLGQKAAPSVTLFPPSSSELQANKATLVCLISDFYPGAVT-----	167
Qy	157	GSTVYVYOGKCLTWKGPRLQPAVVPAPLP	185
Db	168	-----VAMKADSSPVKAGVETTTT	186
RESULT 12			
US-11-054-515-1545			
; Sequence 1545, Application US/11054515			
; Publication No. US20050255532A1			
; GENERAL INFORMATION:			
; APPLICANT: Ruben et al.			
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BlyS			
; FILE REFERENCE: PFS23P3			
; CURRENT APPLICATION NUMBER: US/11/054,515			
; CURRENT FILING DATE: 2005-02-10			
; PRIOR APPLICATION NUMBER: 60/543,296			
; PRIOR FILING DATE: 2004-02-11			
; PRIOR APPLICATION NUMBER: 60/580,347			
; PRIOR FILING DATE: 2004-06-18			
; PRIOR APPLICATION NUMBER: 10/293,418			
; PRIOR FILING DATE: 2002-11-14			
; PRIOR APPLICATION NUMBER: 60/331,469			
; PRIOR FILING DATE: 2001-11-16			
; PRIOR APPLICATION NUMBER: 60/340,817			
; PRIOR FILING DATE: 2001-12-19			
; PRIOR APPLICATION NUMBER: 09/880,748			
; PRIOR FILING DATE: 2001-06-15			
; PRIOR APPLICATION NUMBER: 60/293,499			
; PRIOR FILING DATE: 2001-05-25			
; PRIOR APPLICATION NUMBER: 60/277,379			
; PRIOR FILING DATE: 2001-03-21			
; PRIOR APPLICATION NUMBER: 60/276,248			
; PRIOR FILING DATE: 2001-03-16			
; PRIOR APPLICATION NUMBER: 60/240,816			
; PRIOR FILING DATE: 2000-10-17			
; Remaining Prior Application data removed - See File Wrapper or PALM.			
; NUMBER OF SEQ ID NOS: 3247			
; SEQ ID NO 1545			
; LENGTH: 253			
; TYPE: PRT			
; ORGANISM: Homo sapiens			
US-11-054-515-1545			
Query Match 8.9%; Score 95; DB 7; Length 253;			
Best Local Similarity 25.4%; Pred. No. 0.098;			
Matches 33; Conservative 20; Mismatches 41; Indels 36; Gaps 6			
Qy	15	GSCALWVSQPPERTLEGSSAFPLCSFNASQRLAIGSVTWFRD-----EVPGKEVR	67
Db	141	GSAQSVLTQPPSVSAASGORVTIPCS--GSSNIGISVSWYQQFPGSAPKFLISGNKRP	198
Qy	68	NGTPEFRGRPLAPLASSRFLHDHQAELHIRDVRGHDAIYVCVRVEVLGLGVGT-----	119
Db	199	SGIPD-RFSVSKSGTS-----ATLDTGLGTGDEADYYC-----GTWDTTLNAAW	241
Qy	120	--GNGTRLVV	127
Db	242	VFGAGTKLTV	251
RESULT 13			
US-11-000-463-815			
; Sequence 815, Application US/11000463			

```
; Publication No. US20050266423A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Chen, Rui-hong
; APPLICANT: Qian, Xiaohong B.
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wehrman, Tom
; APPLICANT: Zhang, Jie
; APPLICANT: Zhou, Ping
; APPLICANT: Cao, Yi-Cheng
; APPLICANT: Dmanac, Radoje T.
; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
; FILE REFERENCE: 785CIP4CN
; CURRENT APPLICATION NUMBER: US/11/000,463
; CURRENT FILING DATE: 2004-11-29
; PRIOR APPLICATION NUMBER: 10/291,265
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: PCT/US01/02623
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 09/922,279
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/617,746
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 09/631,451
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 09/633,870
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 944
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 815
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-000-463-815

Query Match      8.9%; Score 94.5; DB 7; Length 236;
Best Local Similarity 22.5%; Pred. No. 0.1;
Matches 48; Conservative 31; Mismatches 77; Indels 57; Gaps 10;

Qy 1 MAMLLLLIMVH--PGSCALW-VSQPPEIRTLGSSAFPLPCSFNASQGRLAIGSVTWFRD 58
Db 1 MAMPLFLGLVAYCTGAVASVELTPQPSVSPQGTASITCSGP-----RLGDKIACYW-- 54
Qy 59 EVVPEK-----EVRNGTPE-PRGR LAPLASSRFLHDHQAELHIRDVRGHDAIYV 107
Db 55 QLKPGQPLVVIHQDTKRPSGIPERFGSNS-----GNTATLTISGTQAMDEADYY 105
Qy 108 CRVEVLGLVGTGNGTRLV-----EKEHPQLGAGTVLLLRAGFYAVSFL 152
Db 106 CQAWDSSSYAFGGGTKLTVLGQPKAAPSVTLFPPSSSEELQANKATLVCLISDFYP-GW 164
Qy 153 SVAVGSTVYVYQKCLTWKGRRLQPAVVPAPLP 185
Db 165 TVA-----WKADSSPVAGVETTP 184

RESULT 14
US-11-062-186-62
; Sequence 62, Application US/11062186
; Publication No. US20050272097A1
; GENERAL INFORMATION:
; APPLICANT: CALENOFF, EMANUEL
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING AND TREATING
; FILE REFERENCE: 21417-98470
; CURRENT APPLICATION NUMBER: US/11/062,186
; CURRENT FILING DATE: 2005-02-18
; PRIOR APPLICATION NUMBER: 60/546,062
; PRIOR FILING DATE: 2004-02-18

; Publication No. US20050266423A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Chen, Rui-hong
; APPLICANT: Qian, Xiaohong B.
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wehrman, Tom
; APPLICANT: Zhang, Jie
; APPLICANT: Zhou, Ping
; APPLICANT: Cao, Yi-Cheng
; APPLICANT: Dmanac, Radoje T.
; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
; FILE REFERENCE: 785CIP4CN
; CURRENT APPLICATION NUMBER: US/11/000,463
; CURRENT FILING DATE: 2004-11-29
; PRIOR APPLICATION NUMBER: 10/291,265
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: PCT/US01/02623
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 09/922,279
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/617,746
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 09/631,451
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 09/633,870
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 944
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 815
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-000-463-815

; PRIOR APPLICATION NUMBER: 60/545,980
; PRIOR FILING DATE: 2004-02-18
; NUMBER OF SEQ ID NOS: 172
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 62
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-062-186-62

Query Match      8.9%; Score 94.5; DB 7; Length 247;
Best Local Similarity 27.3%; Pred. No. 0.11;
Matches 62; Conservative 26; Mismatches 84; Indels 55; Gaps 15;

Qy 5 LLLILLIMV---HPGSCALWVSPPEIRTLGSSAFPLPCSFNASQGRLAIG-SVTWFRDEV 60
Db 17 LLLLLLQVSSSYAGQPRVIGPRHP-IRALVGDEVELPC--RISPGKNATGMEVGWYRP-- 71
Qy 61 VPGKEV-----RNG-----TPEFRGLAPLASSRFLHDHQAELHIRDVRGHDAIYVC- 108
Db 72 -PFSRVVHLRYNGKDDQDQAPRYGRTELLKDA--IGEGKVTLRIRNVRFSDGGFTCF 128
Qy 109 -----RVEVLGLVGTGNGTRLVVEKEHPQLGAGTVLLLRAGFYAVSFLSVAVGSTVYV 162
Db 129 FRDHSYQEEA-----AMELKVEDPPFYWVSGVLVLL--AVLPVLLQLITVGLVFL- 176
Qy 163 QGKCLTWKGRRLQPAVV-----PAPLP PPGCS-SAHLLPPVPG 200
Db 177 ---CLQYR-LRGKLRAEIENLHRTFDPHFLRVPCKITLFIIVPVLG 219

RESULT 15
US-11-033-039-877
; Sequence 877, Application US/11033039
; Publication No. US2006002947A1
; GENERAL INFORMATION:
; APPLICANT: HUMPHREYS, ROBERT
; APPLICANT: XU, MINZHEN
; TITLE OF INVENTION: LI-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES
; FILE REFERENCE: RBH-2017US01
; CURRENT APPLICATION NUMBER: US/11/033,039
; CURRENT FILING DATE: 2005-01-11
; PRIOR APPLICATION NUMBER: 10/245,871
; PRIOR FILING DATE: 2002-09-17
; PRIOR APPLICATION NUMBER: 10/197,000
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: 09/396,813
; PRIOR FILING DATE: 1999-09-14
; NUMBER OF SEQ ID NOS: 1452
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 877
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-033-039-877

Query Match      8.9%; Score 94.5; DB 7; Length 247;
Best Local Similarity 27.3%; Pred. No. 0.11;
Matches 62; Conservative 26; Mismatches 84; Indels 55; Gaps 15;

Qy 5 LLLILLIMV---HPGSCALWVSPPEIRTLGSSAFPLPCSFNASQGRLAIG-SVTWFRDEV 60
Db 17 LLLLLLQVSSSYAGQPRVIGPRHP-IRALVGDEVELPC--RISPGKNATGMEVGWYRP-- 71
Qy 61 VPGKEV-----RNG-----TPEFRGLAPLASSRFLHDHQAELHIRDVRGHDAIYVC- 108
Db 72 -PFSRVVHLRYNGKDDQDQAPRYGRTELLKDA--IGEGKVTLRIRNVRFSDGGFTCF 128
Qy 109 -----RVEVLGLVGTGNGTRLVVEKEHPQLGAGTVLLLRAGFYAVSFLSVAVGSTVYV 162
Db 129 FRDHSYQEEA-----AMELKVEDPPFYWVSGVLVLL--AVLPVLLQLITVGLVFL- 176
Qy 163 QGKCLTWKGRRLQPAVV-----PAPLP PPGCS-SAHLLPPVPG 200
```

Db 177 ---CLQYR-LRGKRAEINLHRTDPHFLRVPCWKITLFIIVPVLG 219

Search completed: February 27, 2006, 18:07:57
Job time : 20 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - nucleic search, **using frame_plus p2n model**

Run on: February 28, 2006, 06:25:45 ; Search time 3393 Seconds
(without alignments)
3367.384 Million cell updates/sec

Title: US-10-696-259-6

Perfect score: 1067

Sequence: 1 MAMLLILILVHPGSCALW.....APLPPPCGSSAHLPLPPVGG 201

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlp
-Q=/abs/ABSSWEB.spool/US10696259/runat_27022006_123555_27124/app.query.fasta_1
-DB=GenEmbl -QWTF=fastap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=spect -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abs03p
-USER=US10696259 @CGN 1 1 7415 @runat_27022006_123555_27124 -NCPU=6 -ICPU=3
-NO MMAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-WAEN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenEmbl.*

1: gb_ba.*
2: gb_in.*
3: gb_env.*
4: gb_on.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pr.*
9: gb_pro.*
10: gb_sts.*
11: gb_sy.*
12: gb_un.*
13: gb_vi.*
14: gb_vtg.*
15: gb_pl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	1067	100.0	1024	8	BC052582 Homo sapi
2	1067	100.0	1061	6	CS032788 Sequence
3	1067	100.0	1061	6	CS041740 Sequence

4	1067	100.0	1061	8	AF031137	AF031137 Homo sapi
5	1051	98.5	789	8	PTRS16006	AJ516006 Pan trogl
6	1039	97.4	834	6	BD087743	BD087743 BMOG, nov
7	1025	96.1	1116	6	CS032897	CS032897 Sequence
8	1025	96.1	1116	6	CS041849	CS041849 Sequence
9	1025	96.1	1116	6	AF031136	AF031136 Homo sapi
10	997	93.4	889	6	BD087742	BD087742 BMOG, nov
c 11	980.5	91.9	1613	10	BV174406	BV174406 sqm71530
12	876	82.1	573	6	AX148159	AX148159 Sequence
13	876	82.1	573	8	AB055881	AB055881 Homo sapi
14	876	82.1	606	6	AX148158	AX148158 Sequence
15	876	82.1	674	6	AX148147	AX148147 Sequence
16	876	82.1	674	8	HS4J3153	AJ223153 Homo sapi
17	876	82.1	874	8	AF031138	AF031138 Homo sapi
c 18	872	81.7	15997	8	CR759886	CR759886 Human DNA
c 19	872	81.7	40160	8	EX248519	EX248519 Human DNA
c 20	872	81.7	55481	8	CR942185	CR942185 Human DNA
c 21	872	81.7	61358	8	AL929587	AL929587 Human DNA
c 22	872	81.7	81800	8	HSY14768	Y14768 Homo sapien
c 23	872	81.7	100409	8	EX927320	EX927320 Human DNA
c 24	872	81.7	101422	8	CR753892	CR753892 Human DNA
c 25	872	81.7	110000	8	BA000025_03	Continuation (4 of
c 26	872	81.7	132330	8	AL662801	AL662801 Human DNA
c 27	872	81.7	135784	8	AL662847	AL662847 Human DNA
c 28	872	81.7	184666	8	DJ201G24	AF129756 Homo sapi
c 29	872	81.7	349980	6	CS039420	CS039420 Sequence
c 30	859	80.5	496	6	CQ730908	CQ730908 Sequence
c 31	853.5	80.0	6853	8	U00921	U00921 Homo sapien
c 32	848	79.5	671	6	BD087741	BD087741 BMOG, nov
c 33	840.5	78.8	110000	8	AB128049	AB128049 Macaca mu
c 34	840.5	78.8	182826	8	AC148688	AC148688 Macaca mu
c 35	827	77.5	612	8	MFA278389	AJ278389 Macaca fa
c 36	826	77.5	616	8	AY035215	AY035215 Macaca mu
c 37	826	77.4	649	8	AY035214	AY035214 Macaca mu
c 38	826	77.4	649	8	MMU554301	AJ554301 Macaca mu
c 39	773	72.4	5581	6	A58551	A58551 Sequence 1
c 40	773	72.4	5581	6	A79836	A79836 Sequence 1
c 41	773	72.4	5581	6	AR182587	AR182587 Sequence
c 42	728	66.2	421	6	AX148156	AX148156 Sequence
c 43	713	66.8	405	6	AX367030	AX367030 Sequence
c 44	713	66.8	1110	6	AX367031	AX367031 Sequence
c 45	707	66.3	542	6	AX778498	AX778498 Sequence

ALIGNMENTS

RESULT 1	BC052582	1024 bp	mRNA	linear	PRI 30-JUN-2004
LOCUS	Homo sapiens natural cytotoxicity triggering receptor 3, mRNA (cdna clone MGC:59970 IMAGE:5934651), complete cds.				
DEFINITION	Homo sapiens natural cytotoxicity triggering receptor 3, mRNA (cdna clone MGC:59970 IMAGE:5934651), complete cds.				
ACCESSION	BC052582				
VERSION	BC052582.1				
KEYWORDS	MGC.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	1 (bases 1 to 1024)				
AUTHORS	Srausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Haieh, F., Statchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stachenko, L., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., McKernan, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettman, M., Madan, A., Rodrigues, S.,				

Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywicki,M.I., Skalska,U., Smailus,D.E., Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

1247732
2 (bases 1 to 1024)
Strausberg,R.
Direct Submission
Submitted (16-MAY-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Daniel McVicar, DBS/NCI
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NIHC), Gaithersburg, Maryland
Web site: http://www.nisc.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov
Akhter,N., Ayele,K., Beckert-Sternberg,S.M., Benjamin,B., Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S., Dietrich,N.L., Guinard,S., Guan,X., Gupta,J., Haghighi,P., Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R., Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C., McDowell,J., Pearson,R., Stantropop,S., Thomas,P.J., Touchman,J.W., Tsurgon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L., Young,A., Zhang,L.-H. and Green,E.D.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAL Plate: 47 Row: f Column: 19
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 24475831.
Location/Qualifiers
1..1024
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="MGC:59970 IMAGE:5934651"
/tissue_type="Blood, natural killer cell"
/clone_lib="NTH MGC 106"
/lab_host="DH10B-R"
/note="Vector: pOTB7"
1..1024
/gene="NCR3"
/note="synonyms: 1C7, NKp30, LY117"
/db_xref="GeneID:259197"
209..814
/gene="NCR3"
/codon_start=1
/product="natural cytotoxicity triggering receptor 3"
/protein_id="AAH52582.1"
/db_xref="GI:30851221"
/db_xref="GeneID:259197"
/translation="MAWMLLLIMVHPGSCALWVSOPPEITLGGSAFLPCSPNAS QRLAIGSVTFRDEVPGKEVRNGTFPRGLAPLASSRFLHQAELHLDVRGHD ASIYCRVGLGVGTGNTKLVVEKEHPQLGAGTVLLLRAGFVAVSLVAVGSTV YYQKCLTKWGPRLQPAVVPAPLPFGSSAHLPPVPGG"

Alignment Scores:
Pred. No.: 7,8e-72 Length: 1024
Score: 1067.00 Matches: 201
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0

ORIGIN
source
1..1061
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

FEATURES
Source
1..1024
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="MGC:59970 IMAGE:5934651"
/tissue_type="Blood, natural killer cell"
/clone_lib="NTH MGC 106"
/lab_host="DH10B-R"
/note="Vector: pOTB7"
1..1024
/gene="NCR3"
/note="synonyms: 1C7, NKp30, LY117"
/db_xref="GeneID:259197"
209..814
/gene="NCR3"
/codon_start=1
/product="natural cytotoxicity triggering receptor 3"
/protein_id="AAH52582.1"
/db_xref="GI:30851221"
/db_xref="GeneID:259197"
/translation="MAWMLLLIMVHPGSCALWVSOPPEITLGGSAFLPCSPNAS QRLAIGSVTFRDEVPGKEVRNGTFPRGLAPLASSRFLHQAELHLDVRGHD ASIYCRVGLGVGTGNTKLVVEKEHPQLGAGTVLLLRAGFVAVSLVAVGSTV YYQKCLTKWGPRLQPAVVPAPLPFGSSAHLPPVPGG"

Query Match: 100.0% Indels: 0
DB: 8 Gaps: 0
US-10-696-259-6 (1-201) x BC052582 (1-1024)
QY 1 MetAlaTriPMeLeuLeuLeuLeuLeuLeuMetValHisProGlySerCysAlaLeuTriP 20
Db 209 ATGGCTGTGATGCTGTGTGCTCATCTTGTATCATGTGTCATCCAGGATCTCTCTCTGG 268
QY 21 ValSerGlnProProGluLeuLeuLeuLeuLeuGlySerSerAlaPheLeuProCysSer 40
Db 269 GTGTCCAGCCCTGAGATTGTTACCTGGAGGATCTCTGCTTCTGCTTCTGCTCTCTCC 328
QY 41 PheAsnAlaSerGlnGlyValGluLeuAlaLeuGlySerValTriPheArgAspGluVal 60
Db 329 TTCAATGCCAGCCAGGAGACTGGCCATTTGCTCGTCACTGGTTCGAGATGAGGTG 388
QY 61 ValProGlyLysGluValArgAsnGlyThrProGluPheArgGlyValGlyValGlyVal 80
Db 389 GTTCCAGGGAAGCAGGTGAGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAAT 448
QY 81 AlaSerSerArgPheLeuHisAspHisGlnAlaGluLeuHisLeuArgAspValArgGly 100
Db 449 GCTTCTCTCCGTTTCTCTCATGACCAACAGGCTGAGCTGCACATCCGGACGTCGAGGC 508
QY 101 HisAspAlaSerIleTyrValCysArgValGluValGluLeuGlyValGlyValGlyVal 120
Db 509 CATGACGCCAGCATCTACGTGTGCAGAGTGGAGGTGCTGGGCTTGGTGTCCGGACAGGG 568
QY 121 AsnGlyThrArgLeuValValGluLysGluHisProGlnLeuGlyAlaGlyThrValLeu 140
Db 569 AATGGACCTCGCTGGTGGTGGAGAAAGAACATCTCAGCTAGGGGGTGTGTACAGTCTCTC 628
QY 141 LeuLeuArgAlaGlyPheTyrAlaValSerPheLeuSerValAlaValGlySerThrVal 160
Db 629 CTCCTTCCGGCTGATTTCTATGCTGTGCTTTCTCTCTGTGGCTGGCGACACCGTC 688
QY 161 TyrTyrGlnGlyLysCysLeuThrTriPLeuGlyProArgArgGlnLeuProAlaValVal 180
Db 689 TATTACCGAGGCAATGCTCTGACCTGGAAGGTCGAAGAGGAGGAGTGGCGGTGTGGTC 748
QY 181 ProAlaProLeuProProProCysGlySerSerAlaHisLeuLeuProProValProGly 200
Db 749 CCAGGCGCCCTCCACCACCATGTGGAGTGCAGCATCTGCTTCTCCCGGACGACCGA 808
QY 201 Gly 201
Db 809 GGC 811
RESULT 2
CS032788 1061 bp DNA linear PAT 10-MAR-2005
LOCUS
DEFINITION
Sequence 2294 from Patent WO2005016962.
CS032788
ACCESSION
CS032788.1 GI:60732157
VERSION
KEYWORDS
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1
REFERENCE
AUTHORS
Abbas,A., Clark,H., Ouyang,W., Williams,M.P., Wood,W.I. and Wu,T.D.
TITLE
Compositions and methods for the treatment of immune related diseases
JOURNAL
Patent: WO 2005016962-A 2294 24-FEB-2005;
Genentech, Inc. (US)
FEATURES
Location/Qualifiers
1..1061
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"


```

Hominidae; Homo.
1 (bases 1 to 1061)
Nalabolu,S.R., Shukla H., Nallur,G., Farimoo,S. and Weissman,S.M.
Genes in a 220-kb region spanning the TNF cluster in human MHC
Genomics 31 (2), 215-222 (1996)
8824804
REFERENCE
2 (bases 1 to 1061)
Nalabolu,S.R., Raghunathan,A. and Weissman,S.M.
Analyses of the transcription pattern of B144 and 1c7, two immune
system related genes encoded near the TNF cluster
Unpublished (1997)
JOURNAL
3 (bases 1 to 1061)
Nalabolu,S.R., Raghunathan,A., Sivakanasundari,R. and Weissman,S.M.
Direct Submission
Submitted (23-OCT-1997) Genetics, Yale School of Medicine, 333
Cedar street, New Haven, CT 06510, USA
JOURNAL
FEATURES
source
1..1061
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/chromosome="6"
/map="6p21.3: MHC complex"
/tissue_type="spleen"
265..870
/note="alternatively spliced; precise translation start
site not known; initiating methionine could also be one of
the next two methionines in the sequence"
/codon_start=1
/product="1c7 precursor"
/protein_id="AAB86579.1"
/db_xref="GI:2623875"
/translation="MAWMLLLILIMVHPGSCALMVSPPEIRTLGGSAFLPCSFNAS
QGRLAIGSVTFWRDEVVPGKEVRNGTPEFRGLAPLASRFLHDHQLHRLDRVRGHD
ASIVYCRVEVLGLGVGTGNGTRLVVEKEHPQLGAGTVLLLRAGFYAVSFSLVAVGSTV
YYQKCLTWKGPRLQPAVVPAPLPPLPPCGSSALLPPVPGG"
265..447
sig_peptide
mat_peptide
448..867
/misc_feature
695..750
/note="encodes putative membrane anchor site"
1003..1008
polyA_signal
ORIGIN
Alignment Scores:
Pred. No.: 8,1e-72 Length: 1061
Score: 1067.00 Matches: 201
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 8 Gaps: 0
US-10-696-259-6 (1-201) x AF031137 (1-1061)
QY 1 MetAlaTrpMetLeuLeuLeuLeuLeuMetValHisProGlySerCysAlaLeuTrp 20
Db 265 ATGGCGCTGGATGCTGTGCTCACTGATCATGGTCCATCCAGGATCTGTGCTCTGG 324
QY 21 ValSerGlnProProGluLeuArgThrLeuGluGlySerSerAlaPheLeuProCysSer 40
Db 325 GTGTCCAGCCCTCGAGATTCGTACCTGGGAAGGATCTCTGCTCTCTGCGCTGCC 384
QY 41 PheAsnAlaSerGlnGlyArgLeuAlaIleGlySerValThrPheArgAspGluVal 60
Db 385 TTCAATGCCAGCAAGGAGACTGCCCATTTGGCTCCGTCCGTCCGTGTTCCGAGATG 444
QY 61 ValProGlyLysGluValArgAsnGlyThrProGluPheArgGlyArgLeuAlaProLeu 80
Db 445 GTTCCAGGAGAGAGGTGAGGAATGGAACCCAGAGTTTCAGGGCGCGCTGCCCACTT 504
QY 81 AlaSerSerArgPheLeuHisAspHisGlnAlaGluLeuHisIleArgAspValArgGly 100
Db 505 GCTTCTCTCCGTTCTCTCCATGACCACCGAGGTGAGTGCACATCCGGACGTGGAGGC 564

```

```

101 HisAspAlaSerIleTyrValCysArgValGluValLeuGlyValGlyThrGly 120
Db 565 CATGACGCCAGCATCTACGTGTGCAGAGTGGAGGTCTGGGCTTGGTGTGGGACAGG 624
QY 121 AsnGlyThrArgLeuValValGluLysGluHisProGlnLeuGlyAlaGlyThrValLeu 140
Db 625 ATGGGACTCGGCTGGTGGTGGAGAAAGAACATCTCAGCTAGGGGCTGGTACAGTCTTC 684
QY 141 LeuLeuArgAlaGlyPheTyrAlaValSerPheLeuSerValAlaValGlySerThrVal 160
Db 685 CTCCTTCGGGCTGGATTTCTATCTGTCACTTCTCTGTGGCGGTGGGACACCGTC 744
QY 161 TyrTyrGlnGlyLysCysLeuThrTrpLysGlyProArgGlnLeuProAlaValVal 180
Db 745 TATTACACGGGCAATGTCTGACCTGGAAGGTTCCAGAGGAGGAGTGGCGCTGTGGTC 804
QY 181 ProAlaProLeuProProCysGlySerSerAlaHisLeuLeuProValProGly 200
Db 805 CCAGCGCCCTCCACCCACCATGTGGAGCTCAGACATCTGCTTCCCGCAGTCCCGGA 864
QY 201 Gly 201
Db 865 GGC 867
RESULT 5
PTRS16006 789 bp mRNA linear PRI 13-NOV-2003
LOCUS Pan troglodytes mRNA for Nkp30 (ncr3 gene).
DEFINITION AJ516006
ACCESSION AJ516006
VERSION AJ516006.1 GI:38322957
KEYWORDS ncr3 gene; Nkp30.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Pan.
REFERENCE 1
AUTHORS Biassoni,R.
TITLE Characterization of natural killer receptors in chimpanzees
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 789)
AUTHORS Biassoni,R.
TITLE Direct Submission
JOURNAL Submitted (13-NOV-2002) Biassoni R., Molecular Immunology, Istituto
Scientifico Tumori, Largo Rosanna Benzi 10, Genova 16132, ITALY
FEATURES
source
1..789
/organism="Pan troglodytes"
/mol_type="mRNA"
/db_xref="taxon:9598"
/tissue_type="lymphoid"
1..789
/gene="ncr3"
52..657
/gene="ncr3"
/function="activating natural cytotoxicity receptor"
/codon_start=1
/evidence=experimental
/product="Nkp30"
/protein_id="CAD56759.1"
/db_xref="GI:38322958"
/translation="MAWMLLLILIMVHPGSCALMVSPPEIRTLGGSAFLPCSFNAS
QGRLAIGSVTFWRDEVVPGKEVRNGTPEFRGLAPLASRFLHDHQLHRLDRVRGHD
ASIVYCRVEVLGLGVGTGNGTRLVVEKEHPQLGAGTVLLLRAGFYAVSFSLVAVGSTV
YYQKCLTWKGPRLQPAVVPAPLPPLPPCGSSALLPPVPGG"
ORIGIN
Alignment Scores:
Pred. No.: 9,57e-71 Length: 789
Score: 1051.00 Matches: 199
Percent Similarity: 99.0% Conservative: 0
Best Local Similarity: 99.0% Mismatches: 2

```


Query Match: 98.5% Indels: 0
DB: 8 Gaps: 0
US-10-696-259-6 (1-201) x PTR516006 (1-789)
Qy 1 MetAlaTrpMetLeuLeuLeuLeuLeuLeuMetValHisProGlySerCysAlaLeuTrp 20
Db 52 ATGGCTGGATGCTGTTCTCATCTTGATCATGTGTCATCCAGGATCTGTGCTCTCGG 111
Qy 21 ValSerGlnProProGluLeuLeuArgThrLeuGluGlySerSerAlaPheLeuProCysSer 40
Db 112 GTGTCCAGCCCTGAGATTCTACCTCGAAGGATCTCTGCTTCTGCTCCCTGCTCC 171
Qy 41 PheAsnAlaSerGlnGlyArgLeuAlaIleGlySerValThrTrpPheArgAspGluVal 60
Db 172 TTCAATGCCAGCCCAAGGAGACTGGCCATTGGCTCCGTCACGTGGTTCCGAGATGAGGTG 231
Qy 61 ValProGlyLysGluValArgAsnGlyThrProGluPheArgGlyValArgLeuAlaProLeu 80
Db 232 GTTCCAGGGAAGGAGGTGAGGAATGAACCCCGAGTTTCAGGGGCGCTCGGCCCACTT 291
Qy 81 AlaSerSerArgPheLeuHisAspHisGlnAlaGluLeuHisIleArgAspValArgGly 100
Db 292 GCTTCTTCCGTTTCTCCATGACCACCAAGCTGAGCTGCACATCCGGGAGCTGGAGGC 351
Qy 101 HisPheAlaSerIleTyrValCysArgValGluValLeuGlyLeuGlyValGlyThrGly 120
Db 352 CATGACGCGCAGCATCTACGTGTGCAGAGTGGAGGTGCTGGGCTTGGTGTGCGGACAGG 411
Qy 121 AsnGlyThrArgLeuValGluValGluGlyHisProGlnLeuGlyAlaGlyThrValLeu 140
Db 412 AATGGGACTCGGGCTGGTGGTGGAGAAAGAAATCTCTCAGCTAGGGGCTGGTACAGTCC 471
Qy 141 LeuLeuArgAlaGlyPheTyrAlaValSerPheLeuSerValAlaValGlySerThrVal 160
Db 472 CTCCTTCGGGCTGGATTCTAGCTGTGCTAGCTTCTCTGTGGCGGTGGGAGCAGCCGTC 531
Qy 161 TyrTyrGlnGlyLysCysLeuThrTrpTyrGlyProArgArgGlnLeuProAlaValVal 180
Db 532 TATTACCAGGGCAATGCTGACCTGGAAAGGTCCAAGAGGAGCTGCCGCTGTGTGTC 591
Qy 181 ProAlaProLeuProProCysGlySerSerAlaHisLeuLeuProProValProGly 200
Db 592 CCAGGCGCCCTCCCAACCATGTGGGAGCTCAGACAGCTGCTTCCCGCCAGTCCCAAG 651
Qy 201 Gly 201
Db 652 GGC 654
RESULT 6
BD087743
LOCUS BD087743
DEFINITION BMOG, novel member of myelin oligodendroglia glycoprotein family,
and utilization thereof for immunomodulation.
ACCSSION BD087743
VERSION BD087743.1 GI:22633353
KEYWORDS JP 2001522589-A/3.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 834)
Browning, J.
BMOG, novel member of myelin oligodendroglia glycoprotein family,
and utilization thereof for immunomodulation
Patent: JP 2001522589-A 3 20-NOV-2001;
BIOGEN INC
OS Homo sapiens (human)
PN JP 2001522589-A/3
PD 20-NOV-2001
PF 06-NOV-1998 JP 2000519987
PR 07-NOV-1997 US 60/064761

PI JEFFREY BROWNING
PC C12N15/09,A61K48/00,A61P37/02,C07K14/47,C07K16/18,C07K19/00,
C12N1/15,
PC C12N1/19,C12N5/10,C12P21/02,C12N15/00,C12N5/00 CC
BMOG, novel member of myelin oligodendroglia glycoprotein CC
family, and
CC utilization thereof for immunomodulation
FH Key Location/Qualifiers
FT source 1..834
FT /organism='Homo sapiens (human)'.
FEATURES
source
1..834
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
ORIGIN
Alignment Scores:
Pred. No.: 8,24e-70 Length: 834
Score: 1039.00 Matches: 200
Percent Similarity: 99.5% Conservative: 0
Best Local Similarity: 99.5% Mismatches: 1
Query Match: 97.4% Indels: 1
DB: 6 Gaps: 0
US-10-696-259-6 (1-201) x BD087743 (1-834)
Qy 1 MetAlaTrpMetLeuLeuLeuLeuLeuMetValHisProGlySerCysAlaLeuTrp 20
Db 66 ATGGCTGGATGCTGTTGCTCATCTTGATCATGTGCTCATCCAGGATCTGTGCTCTCGG 125
Qy 21 ValSerGlnProProGluLeuLeuArgThrLeuGluGlySerSerAlaPheLeuProCysSer 40
Db 126 GTGTCCAGCCCTGAGATTCTGTACCTCGAAGGATCTCTGCTTCTGCTCCCTGCTCC 185
Qy 41 PheAsnAlaSerGlnGlyArgLeuAlaIleGlySerValThrTrpPheArgAspGluVal 60
Db 186 TTCAATGCCAGCCCAAGGAGACTGGCCATTGGCTCCGTCACGTGGTTCCGAGATGAGGTG 245
Qy 61 ValProGlyLysGluValArgAsnGlyThrProGluPheArgGlyValArgLeuAlaProLeu 80
Db 246 GTTCCAGGGAAGGAGTGGAGAAATGGAAACCCAGAGTTTCAG-GGGCGCTGGCCCCACTT 304
Qy 81 AlaSerSerArgPheLeuHisAspHisGlnAlaGluLeuHisIleArgAspValArgGly 100
Db 305 GCTTCTTCCGTTTCTCCATGACCACCAAGCTGAGCTGCACATCCCGGAGCTCGAGGC 364
Qy 101 HisAspAlaSerIleTyrValCysArgValGluValLeuGlyLeuGlyValGlyThrGly 120
Db 365 CATGACGCCAGCATCTACGTGTGCAGAGTGGAGGTGCTGGGCTTGGTGTGCGGACAGGG 424
Qy 121 AsnGlyThrArgLeuValValGluLysGluHisProGlnLeuGlyAlaGlyThrValLeu 140
Db 425 AATGGGACTCGGCTGGTGGTGGAGAAAGAAATCCTCAGCTAGGGGCTGGTACAGTCCCT 484
Qy 141 LeuLeuArgAlaGlyPheTyrAlaValSerPheLeuSerValAlaValGlySerThrVal 160
Db 485 CTCCTTCGGGCTGATTCTATGCTGTGTCAGCTTCTCTGTGGCGGTGGGACAGACCGTC 544
Qy 161 TyrTyrGlnGlyLysCysLeuThrTrpLysGlyProArgArgGlnLeuProAlaValVal 180
Db 545 TATTACCAGGGCAAAATGCTGACCTGGAAAGGTCCAAGAGGAGCTGCGGCTGTGTGTC 604
Qy 181 ProAlaProLeuProProCysGlySerSerAlaHisLeuLeuProProValProGly 200
Db 605 CCAGGCGCCCTCCCAACCATGTGGGAGCTCAGCACATCTGCTTCCCCCAGTCCCAAG 664
Qy 201 Gly 201
Db 665 GGC 667
RESULT 7
CS032897

LOCUS	CS032897	1116 bp	DNA	linear	PAT 10-MAR-2000			
DEFINITION	Sequence 2403 from Patent WO2005016962.							
ACCESSION	CS032897							
VERSION	CS032897.1	GI:60732212						
KEYWORDS	Homo sapiens (human)							
SOURCE	Homo sapiens							
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.							
REFERENCE	1 Abbas, A., Clark, H., Ouyang, W., Williams, M.P., Wood, W. I. and Wu, T.D.							
AUTHORS	Compositions and methods for the treatment of immune related							
TITLE	diseases							
JOURNAL	Patent: WO 2005016962-A 2403 24-FEB-2005;							
	Genentech, Inc. (US)							
FEATURES	Location/Qualifiers							
source	1..1116							
	/organism="Homo sapiens"							
	/mol_type="unassigned DNA"							
	/db_xref="taxon:9606"							
ORIGIN								
Alignment Scores:								
Pred. No.:	1,3e-68	Length:	1116					
Score:	1025.00	Matches:	200					
Percent Similarity:	90.9%	Conservative:	0					
Best Local Similarity:	90.9%	Mismatches:	1					
Query Match:	96.1%	Indels:	19					
DB:	6	Gaps:	1					
US-10-696-259-6 (1-201) x CS032897 (1-1116)								
Qy	1	MetAlaTrpMetLeuLeuLeuLeuLeuLeuMetValHisProGlySerCysAlaLeuTrp	20					
Db	265	ATGGCTGGAGCTGTGCTCATCTTGATCATGTGTCATCCAGGATCTGTGCTCTCGG	324					
Qy	21	ValSerGlnProProGluLeuArgThrLeuGluGlySerSerAlaPheLeuProCysSer	40					
Db	325	GTGTCCCAAGCCCCCTGAGATTCGTACCTGGGAAGATCTCTGCTCTCTGCTCCCTGCTCC	384					
Qy	41	PheAsnAlaSerGlnGlyArgLeuAlaLeuLeuGlySerValThrTrpPheArgAspGluVal	60					
Db	385	TTCAATGCCAGCCAAAGGAGACTGGCCCATGCTCCGTCACGTGTTCGAGATGAGGTG	444					
Qy	61	ValProGlyLysGluValArgAsnGlyThrProGluPheArgGlyArgLeuAlaProLeu	80					
Db	445	GTTCCAGGAAGGAGGTGAGGAATGAAACCCAGAGTTCAGGGGCGCGCTGGCCCACTT	504					
Qy	81	AlaSerSerArgPheLeuHisAspHisGlnAlaGluLeuHisIleArgAspValArgGly	100					
Db	505	GCTTCTTCGCTTCTCCATGACCACCAAGGCTGAGCTGCACATCCGGACGTCGGAGGC	564					
Qy	101	HisAspAlaSerIleTyrValCysArgValGluValLeuGlyLeuGlyValGlyThrGly	120					
Db	565	CATGACGCCAGCATCTACGTGTGCAGAGTGGAGGTGCTGGGCTTGGTGTCCGACAGG	624					
Qy	121	AsnGlyThrArgLeuValValGluLysGluHisProGlnLeuGlyAlaGlyThrValLeu	140					
Db	625	AATGGACTCGCTGGTGGTGGAGAAAGAACATCCTCAGCTAGGGGCTGGTACAGTCCTC	684					
Qy	141	LeuLeuArgAlaGlyPheTyrAlaValSerPheLeuSerValAlaValGlySerThrVal	160					
Db	685	CTCCCTTCGGGCTGGATTCTATGTGTGTCAGCTTCTCTGTGGCCGTGGGACACCGTC	744					
Qy	161	TyrTyrGlnGlyLys-Cys-	166					
Db	745	TATTACCGGGCAATATGCGAAATCTACTCTCCGGATTCCCCCAACTCTGAACCTTTC	804					
Qy	167	-----LeuThrTrpLysGlyProArgGlnLeuProAlaValValProAl	182					
Db	805	CTTTCCACCAAGTCTCACTTGAAGAGTCCAGAAAGGAGCTCCGGCTGTGGTCCAGC	864					

Qy	182	aProLeuProProProCysGlySerXalaHisLeuLeuProProValProGlyGly	201
Db	865	GCCCTCCACCACCATGTGGAGACTCAGACATCTGCTCCCAAGTCCAGGAGGC	922
RESULT 8			
CS041849			
LOCUS	CS041849	1116 bp DNA	linear PAT 22-MAR-2005
DEFINITION	Sequence 2403 from Patent WO2005019258.		
ACCESSION	CS041849		
VERSION	CS041849.1	GI:61849203	
KEYWORDS			
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE			
AUTHORS	Abbas, A., Clark, H., Ouyang, W., Williams, P. M., Wood, W. I. and Wu, T. D.		
TITLE	Compositions and methods for the treatment of immune related diseases		
JOURNAL	Patent: WO 2005019258-A 2403 03-MAR-2005;		
FEATURES	Genentech, Inc. (US)		
source	Location/Qualifiers		
	1..1116		
	/organism="Homo sapiens"		
	/mol_type="unassigned DNA"		
	/db_xref="taxon:9606"		
ORIGIN			
Alignment Scores:			
Pred. No.:	1.3e-68	Length:	1116
Score:	1025.00	Matches:	200
Percent Similarity:	90.9%	Conservative:	0
Best Local Similarity:	90.9%	Mismatches:	1
Query Match:	96.1%	Indels:	19
DB:	6	Gaps:	1
US-10-696-259-6 (1-201) x CS041849 (1-1116)			
Qy	1	MetAlaTrpMetLeuLeuLeuLeuLeuMetValHisProGlySerCysAlaLeuTrp	20
Db	265	ATGCGCTGGATGCTGTGCTCATCTTGATCATGGTCCATCAGGATCTCTGCTCTCTGG	324
Qy	21	ValSerGlnProProGluLeuArgThrLeuGluGlySerSerAlaPheLeuProCysSer	40
Db	325	GTGTCCAGCCGCCCTGAGATTCGTACCTCGAGGATCTCTGCTCTCTGCGCTCTCC	384
Qy	41	PheAsnAlaSerGlnGlyArgLeuAlaIleGlySerValThrTrpPheArgAspGluVal	60
Db	395	TTCAATGCCAGCAAGGAGAGACTGGCCATTCGCTCCGTCAGTGGTTCGAGATCAGGTG	444
Qy	61	ValProGlyLysGluValArgAsnGlyThrProGluPheArgGlyArgLeuAlaProLeu	80
Db	445	GTTCAGGGAAGGAGGTGAGGAATGGAAACCCAGAGTTCAGGGGGCGCTGGCCCCACTT	504
Qy	81	AlaSerSerArgPheLeuHisAspHisGlnAlaGluLeuHisIleArgAspValArgGly	100
Db	505	GCTTCTTCCTGCTTCTCCATGATGACCCAGGCGTGAAGTGCATCCGGGACGTCGAGGC	564
Qy	101	HisAspAlaSerIleTyrValCysArgValGluValLeuGlyLeuGlyValGlyThrGly	120
Db	565	CATGACGCCAGCATCTACGTGTGCAGAGTGGAGGTGCTGGGGCTTGCTGGGACAGGG	624
Qy	121	AsnGlyThrArgLeuValValGluLysGluHisProGlnLeuGlyAlaGlyThrValLeu	140
Db	625	AATGGAGATCGCGCTGTGTGTGGAGAAGAAACATCTCAGCTAGGGGCTGTTACAGTCTC	684
Qy	141	LeuLeuAtgAlaGlyPheTyrAlaValSerPheLeuSerValAlaValGlySerThrVal	160
Db	685	CTCCCTCGGGCTGGATTCTATGCTGTTCAGCTTTCTCTGTGGCCCTGGGACACCGTC	744
Qy	161	TyrTyrGlnGlyLys-Cys-----	166

```
Db 745 TATTACAGGGCAAAATATGCCAAATCTACTCTCTCCGGATTCCCCCAACTCTGAACTTTC 804
Qy 167 -----LeuThrTrpLysGlyProArgGlnLeuProAlaValProAl 182
Db 805 CTTTCCACCAGGTCTGACCTGGAAAGGTCCAAGAAGGCAGCTGCCGCTGTGGTCCCAGC 864
Qy 182 aProLeuProProCysGlySerSerAlaHisLeuLeuProValProGlyGly 201
Db 865 GCCCTCCACCACCATGTGGAGCTCAGCACATCTGCTTCCCTCCAGTCCAGGAGGC 922

RESULT 9
AF031136 1116 bp mRNA linear PRI 18-NOV-1997
LOCUS AF031136 Homo sapiens lC7 precursor, mRNA, alternatively spliced, complete cds.
DEFINITION AF031136.1 GI:2623872
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 1116)
AUTHORS Nalabolu,S.R., Raghunathan,A. and Weisman,S.M.
TITLE Analyses of the transcription pattern of B144 and lC7, two immune system related genes encoded near the TNF cluster
JOURNAL Unpublished (1997)
PUBMED 8824804
REFERENCE 2 (bases 1 to 1116)
AUTHORS Nalabolu,S.R., Raghunathan,A., Sivakamasundari,R. and Weisman,S.M.
TITLE Direct Submission
JOURNAL Submitted (23-OCT-1997) Genetics, Yale School of Medicine, 333 Cedar street, New Haven, CT 06510, USA
FEATURES
source
1. .1116
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/chromosome="6"
/map="6p21.3; MHC complex"
/tissue_type="spleen"
265..798
/notes="alternatively spliced; precise translation start site not known; initiating methionine could also be one of the next two methionines in the sequence"
/codon_start=1
/product="lC7 precursor"
/protein_id="AAB86578.1"
/db_xref="GI:2623873"
/translation="MAWMLLILIMVHPSGALWVSQPPRIETLGSSAFLPSCFNAS QGRLAIGSVTFRDEVVPGKEVRNGTPEFRGLAPLASSRFLHDHQLRHDVVRGHD ASIYCVREVLGLGVGTCNGTRLVVEKEHPQLGAGTVLLLRAGFYAVSFLSVAVGSTV YVQGYAKSTLSGFPQL"
265..447
sig_peptide
448..795
mat_peptide
/product="lC7"
695..750
misc_feature
/notes="encodes putative membrane anchor site"
ORIGIN
Alignment Scores:
Pred. No.: 1.36-68 Length: 1116
Score: 1025.00 Matches: 200
Percent Similarity: 90.9% Conservative: 0
Best Local Similarity: 90.9% Mismatches: 1
Query Match: 96.1% Indels: 19
DB: 8 Gaps: 1
```

```
US-10-696-259-6 (1-201) x AF031136 (1-1116)
Qy 1 MetAlaTrpMetLeuLeuLeuLeuLeuMetValHisProGlySerCysAlaLeuTrp 20
Db 265 ATGGCTGGATGCTGTGGTCTCATCTTGATCATGGTCCATCAGGATCCTGTGCTCTCGG 324
Qy 21 ValSerGlnProProGluLeuLeuArgThrLeuGluGlySerSerAlaPheLeuProCysSer 40
Db 325 GTGTCCAGGCCCTGAGATTGCTGACCTCGAAGGATCCTGTGCTTCTTCCCTGTGCTCC 384
Qy 41 PheAsnAlaSerGlnGlyArgLeuAlaLeuGlySerValThrTrpPheArgAspGluVal 60
Db 385 TTCATGCCAGCCAGGAGACTGGCCATTGGCTTCCTGCTCAGTGGTTCAGATGAGGTG 444
Qy 61 ValProGlyLysGluValArgAsnGlyThrProGluPheArgGlyArgLeuAlaProLeu 80
Db 445 GTTCCAGGGAAGGAGGTGAGGAATGGAACCCAGAGTTTCAGGGGCCCTGGCCCACTT 504
Qy 81 AlaSerSerArgPheLeuHisAspHisGlnAlaGluLeuHisIleArgAspValArgGly 100
Db 505 GCTTCTTCCCGTTTCTCTCCATGACCACAGGCTGAGCTGCACATCCGGGACGTCCGAGGC 564
Qy 101 HisAspAlaSerIleTyrValCysAtgValGluValLeuGlyLeuGlyValGlyThrGly 120
Db 565 CATGACCCAGCATCTACGTGCCAGAGTGGAGTGTGGCCCTTGGTGTGGGACAGGG 624
Qy 121 AsnGlyThrArgLeuValValGluLysGluHisProGlnLeuGlyAlaGlyThrValLeu 140
Db 625 AATGGGACTCGGCTGGTGGTGGAGAAAGACATCCTCAGCTAGGGCTGGTACAGTCTCTC 684
Qy 141 LeuLeuArgAlaGlyPheTyrAlaValSerPheLeuSerValAlaValGlySerThrVal 160
Db 685 CTCCTTCGGCTGGATTCTATGTCTCAGCTTCTCTCTGTGGCCGTGGGACGACGCTC 744
Qy 161 TyrTyrGlnGlyLys-Cys-----
745 TATTACAGGGCAAAATATGCCAAATCTACTCTCTCCGGATTCCCCCAACTCTGAACTTTC 804
167 -----LeuThrTrpLysGlyProArgGlnLeuProAlaValProAl 182
Db 805 CTTTCCACCAGGTCTGACCTGGAAAGGTCCAAGAAGGCAGCTGCCGCTGTGGTCCCAGC 864
Qy 182 aProLeuProProCysGlySerSerAlaHisLeuLeuProValProGlyGly 201
Db 865 GCCCTCCACCACCATGTGGAGCTCAGCACATCTGCTTCCCTCCAGTCCAGGAGGC 922

RESULT 10
BD087742 889 bp DNA linear PAT 27-AUG-2002
LOCUS BD087742 BMOG, novel member of myelin oligodendroglia glycoprotein family, and utilization thereof for immunomodulation.
DEFINITION BD087742
ACCESSION BD087742.1 GI:22633352
KEYWORDS JP 2001522589-A/2.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 889)
REFERENCE
AUTHORS Browning,J.
TITLE BMOG, novel member of myelin oligodendroglia glycoprotein family, and utilization thereof for immunomodulation
JOURNAL Patent: JP 2001522589-A 2 20-NOV-2001; BIOGEN INC
COMMENT OS Homo sapiens (human)
PN JP 2001522589-A/2
PD 20-NOV-2001
PF 06-NOV-1998 JP 2000519987
PR 07-NOV-1997 US 60/064761
PI JEFFREY BROWNING
PC C12N15/09,A61K48/00,A61P37/02,C07K14/47,C07K16/18,C07K19/00, C12N1/15,
```

PC	C12N1/19, C12N1/21, C12N5/10, C12P21/02, C12N15/00, C12N5/00 CC
BMOG	novel member of myelin oligodendroglia glycoprotein CC
CC	family, and
FH	utilization thereof for immunomodulation
FT	Key
FT	source
FT	1.889
FT	Location/Qualifiers
FT	Location/Qualifiers
FT	1.889
FT	/organism="Homo sapiens"
FT	/mol_type="genomic DNA"
FT	/db_xref="taxon:9606"
FEATURES	
source	
ORIGIN	
Alignment Scores:	
Pred. No.:	1.34e-66
Score:	997.00
Percent Similarity:	90.5%
Best Local Similarity:	90.5%
Query Match:	93.4%
DB:	6
US-10-696-259-6 (1-201) x BD087742 (1-889)	
Qy	1 MetAlaTrpMetLeuLeuLeuLeuLeuLeuMetValHisProGlySerCysAlaLeuTrp 20
Db	66 ATGGCTGGATGCTGTTGCTCATCTGATCATGTCCATCCAGGATCCTGTGCTCTCTGG 125
Qy	21 ValSerGlnProProGluIleArgThrIleuGluGlySerSerAlaPheLeuProCysSer 40
Db	126 GTGTCCAGCCGCCCTGAGATCTGTACCTCGAAGGATCCTGTGCTTCTCTGCCCTGTCTCC 185
Qy	41 PheAsnAlaSerGlnGlyArgLeuAlaIleGlySerValThrTrpPheArgAspGluVal 60
Db	186 TTCATGCCAGCCAAAGGAGACTGGCCATTGGCTCCGTTCAGTGGTTCGAGATGAGGTG 245
Qy	61 ValProGlyLysGluValArgAsnGlyThrProGluPheArgGlyArgLeuAlaProLeu 80
Db	246 GTTCCAGGGAAGGAGGTGAGGAATGGAACCCACAGATTTCAG-GGGCGCCTGGCCCCACTT 304
Qy	81 AlaSerSerArgPheLeuHisAspHisGlnAlaGluLeuHisIleArgAspValArgGly 100
Db	305 GCTTCTTTCCGCTTTTCCATGACCACCGAGCTGAGCTGCACATCCGGGACGTCCGAGGC 364
Qy	101 HisAspAlaSerIleTyrValCysArgValGluValLeuGlyLeuGlyValGlyThrGly 120
Db	365 CATGACGCCAGCATCTACGTGTGCAGAGTGGAGTGTCTGGGCTTGGTGTCTGGACAGGG 424
Qy	121 AsnGlyThrArgLeuValValGluLysGluHisProGlnLeuGlyAlaGlyThrValLeu 140
Db	425 AATGGGACTCGCTGGTGGTGGGAAAGAACATCTCAGCTAGGGCTGGTACAGTCTCTC 484
Qy	141 LeuLeuArgAlaGlyPheTyrAlaValSerPheLeuSerValAlaValGlySerThrVal 160
Db	485 CTCCTTCGGGTGGATTCTATGCTGTCTGAGCTTCTCTCTGTGGCGGTGGGACGACCGTC 544
Qy	161 TyrTyrGlnGlyLys-Cys----- 165
Db	545 TATTACCAGGGCAATATGCAAAATCTACTCTCTCCGATTCCCCCAACTCTGAACTTTC 604
Qy	167 -----LeuThrTrpLysGlyProArgArgGlnLeuProAlaValValProAl 182
Db	605 CTTTCCACCAAGTCTGACCTGGAAAGGTCCAAAGAGGAGCTGCGGCTGTGTTCCAGC 664
Qy	182 aProLeuProProProCysGlySerSerAlaHisLeuLeuProProValProGlyGly 201
Db	665 GCCCTCCCAACCATGTGGAGCTCAGACATCTGCTTCTCCCACTGCCAGGAGGC 722
RESULT 11	
BV174406/c	
LOCUS	BV174406
DEFINITION	sgnm71530 Human DNA (Sequenom) Homo sapiens STS genomic, sequence tagged site.
	1613 bp DNA linear STS 10-JUN-2004

BV174406
 BV174406.1 GI:48009713
 STS.
 KEYWORDS
 SOURCE
 ORGANISM
 Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominiidae; Homo.
 1 (bases 1 to 1613)
 Nelson, R.M., Marnellos, G., Kammerer, S., Hoyal, C.R., Shi, M.M.,
 Cantor, C.R. and Braun, A.
 Large-Scale Validation of Single Nucleotide Polymorphisms in Gene
 Regions
 Genome Res. (2004) In press
 COMMENT
 Contact: Andreas Braun
 Pharmaceuticals division
 Sequenom, Inc.
 3395 John Hopkins Court, San Diego, CA 92121, USA
 Tel: 18582029018
 Fax: 18582029020
 Email: abraun@sequenom.com
 Primer A: No primer sequence submitted
 Primer B: No primer sequence submitted
 STS size: 1613.
 FEATURES
 source
 1..1613
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /clone_lib="Human DNA (Sequenom)"
 <1..>1613
 STS
 ORIGIN
 Alignment Scores:
 Pred. No.: 4 53e-65 Length: 1613
 Score: 980.50 Matches: 196
 Percent Similarity: 97.5% Conservative: 1
 Best Local Similarity: 97.0% Mismatches: 4
 Query Match: 91.9% Indels: 3
 DB: 10 Gaps: 0
 US-10-696-259-6 (1-201) x BV174406 (1-1613)
 Qy 1 MetAlaTrpMetLeuLeuLeuLeuLeuLeuLeuMetValHisProGlySerCysAlaLeuTrp 20
 Db 1349 ATGCCCTGGAGTCTGTGCTCATCTTGATCATGGTCCATCAGATCCTGTGCTCTCTGG 1290
 Qy 21 ValSerGlnProGluIleArgThrLeuGluGlySerSerAlaPheLeuProCysSer 40
 Db 1289 GTGTCCAGCCCTGGAGTCTGTACCCCTGGAAGGATCCTCTGCCCTCTCTGCCCTGCTCC 1230
 Qy 41 PheAsnAlaSerGlnGlyArgLeuAlaIleGlySerValThrTrpPheArgAspGluVal 60
 Db 1229 TTCAATGCCAGCCAAAGGAGACTGGCCATTGGCTCCGTCACGTGGTGTCCGAGATGAGGTG 1170
 Qy 61 ValProGlyIysGluValArgAsnGlyThrProGluPheArgGlyArgLeuAlaProLeu 80
 Db 1169 GTTTCAGGGGAAGAGTGTAG--GAAGGAAACCCACAGAGTTCA--GGGCGCCTTGCCCCACTT 1114
 Qy 81 AlaserSerArgPheLeuHisAspHisGlnAlaGluLeuHisIleArgAspValArgGly 100
 Db 1113 GCTTCTTCCGTTTCTTCATGATCACCCAGGCTGAGCTGCACATCCGGGACGTGGAGGC 1054
 Qy 101 HisAspAlaSerIleTyValCysArgValGluValLeuGlyLeuGlyValGlyThrGly 120
 Db 1053 CATGACCCAGCATCTACGTGTGCAGAGTGGAGGTGCTGGGCCTTGGTGTCCGGACAGGG 994
 Qy 121 AsnGlyThrArgLeuValValGluIysGluHisProGlnLeuGlyAlaGlyThrValLeu 140
 Db 993 AATGGGACTCGGTGGTGGGAAAGAACATCTCCTCAGCTAGGGGCTGTGTCAGTCCCTC 934
 Qy 141 Leu-LeuArgAlaGlyPheTrValAlaValSerPheLeuSerValAlaValGlySerThrVa 160

Db 933 CTCCTCTCGGGCTGATTTCTATGCTGTGCTTCTCTCTGTGGCGGTGGCAGACCGT 874
Qy 160 lTyTyTyrGlnGlyLysCysLeuThrTrpLysGlyProArgArgGlnLeuProAlaValVa 180
Db 873 CTATTACCAGGCAAAATGCTGACTGGAAGAGTCCAGAGAGNCAGCTACCGGCTGTGGT 814
Qy 180 lProAlaProLeuProProCysGlySerSerAlaHisLeuLeuProProValProGl 200
Db 813 CCCAGCGCCCTCCACCACCATGTGGAGGCTCAGACATCTGCTTCCCCCAGTCCCAGG 754
Qy 200 YGly 201
Db 753 AGGC 750
RESULT 12
AX148159 573 bp DNA linear PAT 08-JUN-2001
LOCUS Sequence 13 from Patent WO0136630.
ACCESSION AX148159
VERSION AX148159.1 GI:14347072
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Moretta,A., Bottino,C. and Blassoni,R.
TITLE Novel triggering receptor involved in natural cytotoxicity mediated by human natural killer cells, and antibodies that identify the same
JOURNAL Patent: WO 0136630-A 13 25-MAY-2001;
Innate Pharma S.A.S. (FR) ; Universita di Genova (IT)
FEATURES source
1..573
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Alignment Scores:
Pred. No.: 1.21e-57 Length: 573
Score: 876.00 Matches: 173
Percent Similarity: 90.2% Conservative: 2
Best Local Similarity: 89.2% Mismatches: 7
Query Match: 82.1% Indels: 12
DB: 6 Gaps: 2
US-10-696-259-6 (1-201) x AX148159 (1-573)
Qy 1 MetAlaTrpMetLeuLeuLeuLeuLeuLeuMetValHisProGlySerCysAlaLeuTrp 20
Db 1 ATGGCCTGGATCGTGTGCTCATCTTGATCATGTCATCCAGGATCTGTGCTCTCTGG 60
Qy 21 ValSerGlnProProGluLeuArgThrLeuGluGlySerSerAlaPheLeuProCysSer 40
Db 61 GTGTCCAGCCCTCGAGATCGTACCTCGGAGGATCCTCTGCTTCTTCCCTGCTCTCC 120
Qy 41 PheAlaSerGlnGlyArgLeuAlaIleGlySerValThrTrpPheArgAspGluVal 60
Db 121 TTCATGCCAGCCAGGAGACTGGCCATTCGCTCCGCTCAGCTGTTCCGAGATGAGGTG 180
Qy 61 ValProGlyLysGluValArgAsnGlyThrProGluPheArgGlyArgLeuAlaProLeu 80
Db 181 GTTCCAGGAGAGAGGTGAGGATGGAAACCCAGAGTTACGGGGCCGCTGGCCCACTT 240
Qy 81 AlaSerSerArgPheLeuHisAspHisGlnAlaGluLeuHisIleArgAspValArgGly 100
Db 241 GCCTTCTCCGCTTCTCCATGACCAACAGGCTGAGCTGCACATCCGGGAGCTCGAGGC 300
Qy 101 HisAspAlaSerIleTyValCysArgValGluValLeuGlyLeuGlyValGlyThrGly 120

Db 301 CATGACCCAGCATCTACGTGTGCAGAGTGGAGGTGCTGGGCCCTTGTGTGGGACAGGG 360
Qy 121 AsnGlyThrArgLeuValValGluLysGluHisProGlnLeuGlyAlaGlyThrValLeu 140
Db 361 AATGGGACTCGGCTGGTGGTGGAGAAAGAACATCTCAGCTAGGGGCTGGTACAGTCTC 420
Qy 141 LeuLeuArgAlaGlyPheTyAlaValSerPheLeuSerValAlaValGlySerThrVal 160
Db 421 CTCCTTCGGGCTGGAATCTATGCTGTCTCTCTCTGTGGCGGTGGGAGCACCGCTC 480
Qy 161 TyTyTyrGlnGlyLys-----CysLeuThrTrpLysGlyPro 172
Db 481 TATTACCAGGCAAAATGCCACTGTGCATGGGAACACACTGCCACTCTCAGATGGGCC 540
Db 541 CGA-----GGGTGATTCAGAGCCAGATGTCCT 570
RESULT 13
AB055881 573 bp mRNA linear PRI 01-DEC-2001
LOCUS Homo sapiens NKp30 mRNA for natural killer cell receptor, complete cds
DEFINITION
ACCESSION AB055881
VERSION AB055881.1 GI:17221621
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Sato,M., Yabe,T., Ohashi,J., Tsuchiya,N., Hanaoka,K., Tokunaga,K. and Juji,T.
TITLE Identification of two novel single nucleotide polymorphisms in the NKp30 gene in human natural killer cells
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 573)
AUTHORS Sato,M.
TITLE Direct Submission
JOURNAL Submitted (15-FEB-2001) Masako Sato, Japanese Red Cross Central Blood Center, Department of Research; Hiroo4-1-31, Shibuya-ku, Tokyo 150-0012, Japan (E-mail:masako@cbc.jrc.or.jp, Tel:81-3-5485-6004, Fax:81-3-3406-7892)
FEATURES source
1..573
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/chromosome="6"
/map="6p21.3"
/tissue_type="peripheral blood"
1..573
/genes="NKp30"
1..573
/genes="NKp30"
/codon_start=1
/product="natural killer cell receptor"
/protein_id="BAB78472.1"
/db_xref="GI:17221622"
translation="MAWMLLLILIMVHPGSCALWVSQPPEIRTEGSSAFLPSCFNAS QSLATGVTWFRDEVPGKEVNGTPEFRRLAPLASSRFLHDHQAELHLDVRGHD ASLYVCRVEVLGVTGNGCTRLVSKHPQLGAGTVLLLRAGFYAVSFLSVAVGSTV YGQKCHMGTHCHSSDGRGVIPEPRCF"
variation 111
/genes="NKp30"
/replace="a"
variation 156
/genes="NKp30"
/replace="t"
ORIGIN
Alignment Scores:


```
/organism="Homo sapiens"  
/mol_type="unassigned DNA"  
/db xref="taxon:9606"
```

ORIGIN

Alignment Scores:			
Pred. No.:	1.45e-57	Length:	674
Score:	876.00	Matches:	173
Percent Similarity:	90.2%	Conservative:	2
Best Local Similarity:	89.2%	Mismatches:	7
Query Match:	82.1%	Indels:	12
DB:	6	Gaps:	2
US-10-696-259-6 (1-201) x AX148147 (1-674)			
QY	1	MetAlaTrpMetLeuLeuLeuLeuLeuLeuMetValHisProGlySerCysAlaLeuTrp	20
DB	64	ATGGCTTGGATGCTGTGCTCATCTTGATCATGGTCCATCCAGGATCCTGTGCTCTCTGG	123
QY	21	ValSerGlnProProGluIleArgThrLeuGluGlySerSerAlaPheLeuProCysSer	40
DB	124	GNGTCCAGCCCCCTGAGATTGCTACCTCTGGAAGGATCCTCTGCCTTCCTGCCCTGCTCC	183
QY	41	PheAsnAlaSerGlnGlyArgLeuAlaIleGlySerValThrTrpPheArgAspGluVal	60
DB	184	TTCAATGCCAGCAAGGAGAGCTGCCATTGGCTCCGTACGTGGTTCCGAGATGAGGTG	243
QY	61	ValProGlyLysGluValArgAsnGlyThrProGluPheArgGlyArgLeuAlaProLeu	80
DB	244	GTTTCAGGGAAGAGGTGAGGAATGGAAACCCAGAGTTTCAGGGGGCGCTGGCCCCCACTT	303
QY	81	AlaSerSerArgPheLeuHisAspHisGlnAlaGluLeuHisIleArgAspValArgGly	100
DB	304	GTCTTCTCCGTTTCTCTCATGACCAACAGGCTGAGTGCACATCCGGGACGTGCAGGC	363
QY	101	HisAspAlaSerIleTyrValCysArgValGluValLeuGlyLeuGlyValGlyThrGly	120
DB	364	CATGACGCCAGCATCTACGTGTGCAGAGTGAGGTGTGGGCCCTTGGTGTGGGACAGG	423
QY	121	AsnGlyThrArgLeuValValGluLysGluHisProGlnLeuGlyAlaGlyThrValLeu	140
DB	424	AATGGGATCTCGCTGCTGTGGAGAAACATCTCAGTAGGGGGTGGTACAGTCCTC	483
QY	141	LeuLeuArgAlaGlyPheTyrAlaValSerPheLeuSerValAlaValGlySerThrVal	160
DB	484	CTTCCTTCGGGCTGGATTCATGCTGTACCTTTCTCTGTGGCCGTGGGCAGCACCGTC	543
QY	161	TyrTyrGlnGlyLys-----CysLeuThrTrpLysGlyPro	172
DB	544	TATTAACAGGGCAATGCCACTGTGCATGGGAACACATGCCCACTCCTCAGATGGGCC	603
QY	173	ArgArgGlnLeuProAlaValValProAlaProLeuProPro	186
DB	604	CGA-----GGRGTTATTCAGAGCCAGATGTGCC	633

Search completed: February 28, 2006, 10:53:02
Job time : 3400 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: February 28, 2006, 06:20:29 ; Search time 588 Seconds
(without alignments)
2278.237 Million cell updates/sec

Title: US-10-696-259-6

Perfect score: 1067

Sequence: 1 MAMWLLILIVHVGSCALW.....APLPFGCSAHLPPVPGG 201

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh
-Q=/abs/ABSSWEB_spool/US10696259/runat_27022006_123553_27112/app_query.fasta.1
-DB-N Geneseq -QFMT=fastap -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=biocum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000 -HOST=abs08
-USR=US10696259 @CGN 1 1 727 @runat_27022006_123553_27112 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WAE TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOF=6 -FGAPEXT=7
-YGAPOF=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

N Geneseq 21.*

- 1: geneseqn1980s.*
- 2: geneseqn1990s.*
- 3: geneseqn2000s.*
- 4: geneseqn2001as.*
- 5: geneseqn2001bs.*
- 6: geneseqn2002as.*
- 7: geneseqn2002bs.*
- 8: geneseqn2003as.*
- 9: geneseqn2003bs.*
- 10: geneseqn2003cs.*
- 11: geneseqn2003ds.*
- 12: geneseqn2004as.*
- 13: geneseqn2004bs.*
- 14: geneseqn2005as.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1067	100.0	606	14	ADV43954 Human psy
2	1067	100.0	606	14	Aea40217 Human nat
3	1067	100.0	1061	14	Adx01458 Human tol
4	1067	100.0	1061	14	ADY16488 DNA encod

5	1039	97.4	834	2	AAX59349	Aax59349 Human B-c
6	1025	96.1	1116	14	ADY16597	Ady16597 DNA encod
7	997	93.4	889	2	AAX59348	Aax59348 Human B-c
8	876	82.1	573	12	ADO19809	Ado19809 Human PRO
9	876	82.1	606	4	AAD06569	Aad06569 Human Nkp
10	876	82.1	674	4	AAD06564	Aad06564 Human Nkp
11	872	81.7	22173	12	ADQ59392	Adq59392 Human can
12	872	81.7	22173	14	ADZ13655	Adz13655 Human can
13	872	81.7	81800	6	ABK84756	Abk84756 Human cdN
c 14	853.5	80.0	6853	14	ADW38506	Adw38506 Immunomod
15	848	79.5	671	2	AAX59347	Aax59347 Human B-c
c 16	773	72.4	5581	2	AAT45451	Aat45451 Human LST
c 17	773	72.4	5581	2	AAT48737	Aat48737 Human leu
18	728	68.2	421	4	AAD06567	Aad06567 Human Nkp
19	713	66.8	405	6	AAD30466	Aad30466 Human Nkp
20	713	66.8	1110	6	AAD30467	Aad30467 Human Nkp
21	707	66.3	542	10	ADF80099	Adf80099 Leukaemia
22	608.5	57.0	1164	12	ADP48757	Adp48757 Human Nkp
23	608.5	57.0	1164	14	AEA40218	Aea40218 DNA encod
24	488	45.7	559	13	ADU12101	Adu12101 Solid tum
25	225.5	21.1	21781	12	ADQ59389	Adq59389 Human can
26	225.5	21.1	21781	14	ADZ13652	Adz13652 Marine ca
27	131.5	12.3	967	10	AAD59187	Aad59187 Human Ig
28	126.5	11.9	44075	9	ADA02774	Ada02774 Human ARH
29	126.5	11.9	44075	10	ADB72512	Adb72512 Human ARH
30	126.5	11.9	44075	10	ADC85254	Adc85254 Human Arh
31	126.5	11.9	44075	12	ADM74369	Adm74369 Human car
32	125.5	11.8	869	6	AAQ70451	Aaq70451 DNA encod
33	125	11.7	636	2	AAT08531	Aat08531 Full leng
34	125	11.7	636	2	AAT29989	Aat29989 DNA encod
35	125	11.7	636	2	AAV69786	Aav69786 Human CTL
36	125	11.7	636	2	AAV83670	Aav83670 Human CTL
37	125	11.7	636	6	ABQ78361	Abq78361 Nucleotid
38	125	11.7	636	6	ABQ78361	Abq78361 Nucleotid
39	125	11.7	636	6	ABQ78361	Abq78361 Nucleotid
40	125	11.7	636	8	ABZ22582	Abz22582 DNA encod
41	125	11.7	636	10	ADD89012	Add89012 CTLA4 rec
42	125	11.7	636	12	ADQ89551	Adq89551 CTLA4 rec
43	125	11.7	636	12	ADP95981	Adp95981 Human CTL
44	125	11.7	636	14	ADW98654	Adw98654 Human CTL
45	125	11.7	636	14	ADX08913	Adx08913 DNA encod

ALIGNMENTS

RESULT 1

ADV43954

ID ADV43954 standard; cDNA; 606 BP.

XX AC ADV43954;

XX AC

DT 10-MAR-2005 (first entry)

XX DT

DE Human psychoneuroendocrinimmune expressed sequence tag SEQ ID NO 1582.

XX DE

KW microarray; psychoneuroendocrinimmune; chronic fatigue;

KW non-insulin dependent diabetes; allergy; immune disorder; inflammation;

KW cancer; neoplasm; infection; expressed sequence tag; ss.

XX KW

OS Homo sapiens.

XX OS

FN WO2004108899-A2.

XX FN

PD 16-DEC-2004.

XX PD

PF 04-JUN-2004; 2004WO-US017686.

XX PF

PR 04-JUN-2003; 2003US-0475915P.

XX PR

PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX PA

XX Nicholson A, Vernon SD;

XX PI

DR WPI; 2005-031682/03.

XX New microarray comprising probes for genes involved in

PT psychoneuroendocrine (PNI) activity, useful in diagnosing a

PT condition associated with PNI activity, e.g., inflammatory or infectious

PT diseases.

XX Claim 1; SEQ ID NO 1582; 254pp; English.

PS The invention relates to a new microarray which comprises probes for

XX genes involved in psychoneuroendocrine (PNI) activity. The

CC microarray is useful in diagnosing a condition associated with PNI

CC activity, such as CFS, type-2 diabetes, allergic condition, inflammation,

CC cancer and infection. The present sequence represents a

CC psychoneuroendocrine gene expressed sequence tag. Note the

CC specificatio mentions SEQ ID NO of up to 3314 but only sequences up to

XX SEQ ID NO 1829 are provided.

XX

SQ Sequence 606 BP; 105 A; 182 C; 184 G; 135 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 2.26e-85 Length: 606

Score: 1067.00 Matches: 201

Percent Similarity: 100.0% Conservative: 0

Best Local Similarity: 100.0% Mismatches: 0

Query Match: 100.0% Indels: 0

DB: 14 Gaps: 0

US-10-696-259-6 (1-201) x ADV43954 (1-606)

QY 1 MetAlaTrpMetLeuLeuLeuLeuLeuMetValHisProGlySerCysAlaLeuTrp 20

Db 1 ATGGCTGGATGCTGGTGGTCACTTGTATCATGTCATCCAGATCTGCTGCTCTGG 60

QY 21 ValSerGlnProProGluLeuLeuArgThrLeuGluGlySerSerAlaPheLeuProCysSer 40

Db 61 GTGTCCCGAGCCCTGAGATTCTGATCCCTGGAAGGATCTCTGCTTCTGCTGCTGCTCC 120

QY 41 PheAlaSerGlnGlyArgLeuAlaLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 60

Db 121 TTCAATGCCACCCAGGAGAGTGGCCATTTGGCTCCGTCACGTGGTTCGAGATGAGGTG 180

QY 61 ValProGlyLysGluValArgAsnGlyThrProGluPheArgGlyValArgLeuAlaProLeu 80

Db 181 GTTCAGGAGAGGAGTGGAGATGGAAACCCAGATTACAGGGCGGCTGCCCCACTT 240

QY 81 AlaSerSerArgPheLeuHisAspHisGlnAlaGluLeuHisLeuAlaValArgGly 100

Db 241 GCTTCTTCCCGTTCTCTCATGACCCAGCCAGCTGAGCTGCATCCGGAGCTGGAGGC 300

QY 101 HisAlaPheLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 120

Db 301 CATGACGCCAGCATCTACGTGTGCAGATGGAGGTGCTGGGCTTGGTTCGGGACAGGG 360

QY 121 AsnGlyThrArgLeuValValGluLysGluHisProGlnLeuGlyValAlaGlyThrValLeu 140

Db 361 AATGGGATCTCGGCTGGTGGTGGAGAAAGACATCTCTAGTAGGGGCTGTACAGTCTC 420

QY 141 LeuLeuArgAlaGlyPheTyAlaValSerPheLeuSerValAlaValAlaGlySerThrVal 160

Db 421 CTCCCTCGGGCTGGATTTCTATGCTGTACGCTTCTCTGTGTGGCGCTGGGACAGCCGTC 480

QY 161 TyrTyrGlnGlyLysCysLeuThrTrpLysGlyProArgArgGlnLeuProAlaValVal 180

Db 481 TATTACAGGGAATGTCTGACCTGGAAAGTCCAAAGGACAGCTGCCGCTGTGGTC 540

QY 181 ProAlaProLeuProProProCysGlySerSerAlaHisLeuLeuProProValProGly 200

Db 541 CCAGGCCCTCCACCCACCATGTGGAGCTCAGCACATCTCTCTCTCTCTCTCTCTCTCTCT 600

QY 201 Gly 201

Db 601 GGC 603

RESULT 2

AEA40217

ID AEA40217 standard; DNA; 606 BP.

XX

AC AEA40217;

XX

DT 11-AUG-2005 (first entry)

XX

DE Human natural cytotoxicity receptor associated DNA, SEQ ID No:23.

XX

XX natural cytotoxicity receptor; natural killer cell; lymphocyte; membrane;

KW tumor; cell disintegration; antibody; hyperproliferation; cytostatic; ds.

XX

OS Homo sapiens.

XX

PN WO2005051973-A2.

XX

XX 09-JUN-2005.

XX

XX 24-NOV-2004; 2004WO-IL001081.

XX

PR 25-NOV-2003; 2003US-0524648P.

XX

PA (YISS) YISSUM RES & DEV CO.

PA (UYNE) UNIV BEN-GURION NEGEV RES & DEV.

XX

XX Mandelboim O, Porgador A;

PI

XX

XX WPI; 2005-405348/41.

XX

XX New peptides derived from specific natural cytotoxicity receptors and

PT capable of binding to membrane-associated biomolecules of tumor cells,

PT useful for targeting tumor cells to diagnose or treat benign and/or

PT malignant tumors.

XX

PS Disclosure; SEQ ID NO 23; 86pp; English.

XX

XX The invention relates to isolated peptide fragments of a natural

CC cytotoxicity receptor (NCR) of natural killer (NK) cells, or active

CC fragments, analogs or derivatives, wherein the peptide fragment is

CC capable of binding to a membrane-associated biomolecule of a tumor cell,

CC and the biomolecule comprises at least one sulfated polysaccharide, and

CC serves as the binding site of the NCR mediating the lysis of tumor cells

CC by NK cells, with the proviso that the peptide is other than a full

CC length NCR polypeptide or an isolated NCR extracellular domain. Also

CC described are: (1) an antibody that recognizes an epitope on a target

CC membrane-associated biomolecule of a tumor cell, the biomolecule

CC comprising at least one sulfated polysaccharide and mediating the lysis

CC of tumor cells by NK cells via the NCR; (2) a method of targeting a tumor

CC cell in a subject via an NCR-dependent mechanism; and (3) a method of

CC identifying peptides derived from NCR which are capable of binding to a

CC membrane-associated sulfated polysaccharide of a tumor cell. The peptide

CC fragment comprises 7-120, 8-100 or less than about 50 contiguous amino

CC acids. The peptide is a fragment of NCR selected from Nkp44, Nkp30 and

CC NKp46. It is a fragment of the D2 domain of Nkp46 comprising a sequence

CC fully defined in the specification (SEQ ID NOS: 1 and 2), or a fragment

CC of NKp30 selected from a sequence fully defined in the specification (SEQ

CC ID NOS: 3 and 4). Alternatively, the peptide is a fragment of NKp44

CC having a sequence fully defined in the specification (SEQ ID NO: 5). The

CC membrane-associated biomolecule is selected from a glycosaminoglycan and

CC a proteoglycan. The antibody is capable of blocking the binding of NK

CC cells via NCR to membrane-associated sulfated polysaccharide biomolecules

CC in a cell, therefore, inhibiting NCR-dependent cell lysis associated with

CC autoimmunity. The peptides and antibodies of the invention are useful for

CC targeting a tumor cell in a subject via an NCR-dependent mechanism. The

CC composition and methods of the invention are useful for targeting tumor

CC cells to diagnose and/or treat benign and malignant tumors or

CC proliferative diseases. This sequence represents DNA of unknown function

CC relating to the present invention. Note: This sequence given as SEQ ID

CC No:23 in the Sequence Listing is not mentioned elsewhere in the

CC specification.

XX

SQ Sequence 606 BP; 105 A; 182 C; 184 G; 135 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 2,26e-85 Length: 606
Score: 1067.00 Matches: 201
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 14 Gaps: 0

US-10-696-259-6 (1-201) x AEA40217 (1-606)

QY 1 MetAlaTrpMetLeuLeuLeuLeuLeuLeuMetValHisProGlySerCysAlaLeuTrp 20
Db 1 ATGGCTGGATGCTGTCTCATCTTGATCATGTGTCATCCAGGATCCTGTGCTCTCTGG 60
QY 21 ValSerGlnProGluLeuLeuArgThrLeuGluGlySerSerAlaPheLeuProCysSer 40
Db 61 GTGTCCAGCCCTTGAGATTGCTACCTGGAAGGATCCTCTGCTTCTGCTGCTGCTCC 120
QY 41 PheAsnAlaSerGlnGlyArgLeuAlaIleGlySerValThrTrpPheArgAspGluVal 60
Db 121 TTCAATGCCACCAAGGAGACTGGCCATTGGCTCCGTCACGTGGTTCGAGATGAGTG 180
QY 61 ValProGlyLysGluValArgAsnGlyThrProGluPheArgGlyArgLeuAlaProLeu 80
Db 181 GTTCAGGGAAGGAGGTGAGGAATGGAACCCACAGATTTCAGGGCCGCTGGCCCACTT 240
QY 81 AlaSerArgPheLeuHisAspHisGlnAlaGluLeuHisIleArgAspValArgGly 100
Db 241 GCCTTCTCCCGTTTCCCTCATGACACACAGGCTGAGCTGCACATCCGGGACGTGGAGGC 300
QY 101 HisAspAlaSerIleTyrValCysArgValGluValLeuGlyLeuGlyValGlyThrGly 120
Db 301 CATGAGCCAGCATCTAGCTGTGAGAGTGAGGTGCTGGGCCCTTGGTTCGGACAGGG 360
QY 121 AsnGlyThrArgLeuValGluGlyHisProGlnLeuGlyAlaGlyThrValLeu 140
Db 361 AATGGAGCTCGCTGTGTGGTGGAGAAAGAACATCTCAGCTAGGGCTGGTACAGTCTCTC 420
QY 141 LeuLeuArgAlaGlyPheTyrAlaValSerPheLeuSerValAlaValGlySerThrVal 160
Db 421 CTCCTTCGGGCTGGAATTCTATGCTGTCTGAGCTTCTCTGTGGCGCTGGGACAGCCGTC 480
QY 161 TyrTyrGlnGlyLysCysLeuThrTriPlysglyProArgGlnLeuProAlaValVal 180
Db 481 TATTACAGGGCAATGTCTGACCTGGAAAGGTCCAGAGGAGCTGCGGCTGTGTC 540
QY 181 ProAlaProLeuProProProCysGlySerSerAlaHisLeuLeuProProValProGly 200
Db 541 CCAGGCCCCCTCCACCACCATGTGGGAGCTCAGACATCTGCTTCCCCCAGTCCAGGA 600
QY 201 Gly 201
Db 601 GGC 603

RESULT 3

ADX01458
ID ADX01458 standard; DNA; 1061 BP.

AC ADX01458;

DT 21-APR-2005 (first entry)

XX Human tolerance target molecule #31.

DE Screening; immune disorder; autoimmune disease; transplant rejection;
KW diabetes mellitus; arthritis; rheumatoid arthritis; multiple sclerosis;
KW myasthenia gravis; systemic lupus erythematosus; Hashimoto's disease;
KW dermatitis; psoriasis; ulcerative colitis; scleroderma;
KW female genital tract inflammation; Crohn's disease; sarcoidosis;
KW pulmonary fibrosis; immunosuppressive; antidiabetic; antiarthritic;
KW antirheumatic; neuroprotective; muscular-gen.; antiinflammatory;

KW dermatological; antithyroid; antipsoriatic; antiulcer;
KW gastrointestinal-gen.; respiratory-gen.; cytostatic; virucide; gene; ds.
OS Homo sapiens.

XX WO2005010215-A2.

XX 03-FEB-2005.

XX 19-JUL-2004; 2004WO-US023309.

XX 17-JUL-2003; 2003US-0488502P.

XX (TOLE-) TOLERRX INC.

XX Rao P, Snyder J, Bagley A;

XX WPI; 2005-123168/13.

XX Identifying a tolerance modulatory compound, useful for reducing T
effector (Teff) cell function or increasing T regulatory (Treg) cell
function, by assaying for expression or activity of Treg marker and Teff
marker.

XX Disclosure; SEQ ID NO 31; 149pp; English.

XX The invention relates to a method of identifying a tolerance modulatory
compound comprising assaying for expression or activity of at least one T
regulatory (Treg) marker and at least one T effector (Teff) marker, where
a change in expression or activity of the Treg marker or the Teff marker
and/or an inverse change in expression or activity of the Teff marker
identifies the test compound as a tolerance modulatory compound. The
method comprises contacting a T cell with a stimulating agent and a test
compound and assaying for expression or activity of at least one Treg
marker and at least one Teff marker. The invention also relates to a
method of identifying a tolerance promoting compound and a method of
identifying a tolerance suppressing compound. The method is useful for
identifying a tolerance modulatory compound, e.g. a tolerance promoting
compound or a tolerance suppressing compound. The methods are useful for
reducing T effector cell function or for increasing T regulatory cell
function. The modulator identified can be used in an animal model to
determine the efficacy, toxicity or side effects of treatment with the
modulator. Tolerance modulatory compounds are also useful for treating
immune-mediated diseases, e.g. autoimmune diseases, transplant rejection
or unwanted immune responses to chronically administered therapeutic
proteins. Diseases include diabetes mellitus, arthritis, rheumatoid
arthritis, multiple sclerosis, myasthenia gravis, systemic lupus
erythematosus, Hashimoto's disease, dermatitis, psoriasis, ulcerative
colitis, scleroderma, female genital tract inflammation, Crohn's disease,
sarcoidosis and pulmonary fibrosis. The compounds are further useful for
enhancing immune responses, e.g. to tumors or viruses to which the body
may have become tolerant. This sequence represents a human tolerance
target molecule of the invention.

XX SQ Sequence 1061 BP; 212 A; 320 C; 288 G; 241 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 4.46e-85 Length: 1061
Score: 1067.00 Matches: 201
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 14 Gaps: 0

US-10-696-259-6 (1-201) x ADX01458 (1-1061)

QY 1 MetAlaTrpMetLeuLeuLeuLeuLeuMetValHisProGlySerCysAlaLeuTrp 20

Db 265 ATGGCTGGAGTGTGTGCTCATCTTGATCATGTGTCATCCAGGATCCTGTGCTCTCTGG 324

QY 21 ValSerGlnProGluLeuLeuArgThrLeuGluGlySerSerAlaPheLeuProCysSer 40

Db 325 GTGTCCAGGCCCTTGAGATTCGTACCTCGAAGGATCCTCTGCTTCTGCTGCTGCTCC 384

DE Human B-cell myelin oligodendrocyte glycoprotein BMOG cDNA.

KW MBOG; B-cell myelin oligodendrocyte glycoprotein; human;
 KW signal transduction; immunomodulator; antiinflammatory;
 KW autoimmune disease; inflammation; gene therapy; diagnosis; ss.
 OS Homo sapiens.

XX Key Location/Qualifiers

FT CDS 66..670

FT /tag= a

FT /transl_except= (pos:291..292, aa:Arg)

FT /note= "this codon contains an apparent 1 nucleotide

FT deletion, which alters the reading frame"

FT sig_peptide 66..101

FT /tag= b

FT mat_peptide 102..667

FT /tag= c

XX WO9923867-A2.

XX 20-MAY-1999.

XX 05-NOV-1998; 98WO-US023826.

XX 07-NOV-1997; 97US-0064761P.

XX (BIOJ) BIOGEN INC.

XX Browning J;

XX WPI; 1999-418423/35.

XX P-PSDB; AAY06403.

XX Novel B-cell myelin oligodendrocyte glycoproteins.

XX Claim 1; Page 42; 43pp; English.

XX This DNA sequence encodes human BMOG, a novel member of the B cell myelin
 CC oligodendrocyte glycoprotein family that is expressed by germinal centre
 CC B cells. 3 C-terminal splice variants (see AAY06401-03) of BMOG were
 CC identified. The protein is present primarily in the spleen, in lymph
 CC nodes and in germinal centre B cells. It may have immunoregulatory
 CC functions, and soluble or chimeric fusion proteins of BMOG may be used to
 CC regulate the immune system in autoimmune or inflammatory disease. Vectors
 CC comprising BMOG, prokaryotic and eukaryotic host cells, and a method of
 CC producing BMOG using these transformed host cells are also provided. BMOG
 CC polypeptides can be used for modulating the immune system of a subject or
 CC to inhibit signal transduction in a cell expressing BMOG by contacting it
 CC with a soluble BMOG protein. The nucleic acid can be used for gene
 CC therapy. The protein can also be used to target a toxin, imaging agent or
 CC radionuclide to a cell expressing BMOG. (All claimed)

SQ Sequence 834 BP; 152 A; 258 C; 232 G; 192 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1.01e-82 Length: 834

Score: 1039.00 Matches: 200

Percent Similarity: 99.5% Conservative: 0

Best Local Similarity: 99.5% Mismatches: 1

Query Match: 97.4% Indels: 1

DB: 2 Gaps: 0

US-10-696-259-6 (1-201) x AAX59349 (1-834)

Qy 1 MetAlaTrpMetLeuLeuLeuLeuLeuMetValHisProGlySerCysAlaLeuTrp 20

Db 66 ATGGCTGGATGCTGTTCTCATCTGATCATGTGTCATCCAGGATCTGTGCTCTCG 125

Qy 21 ValSerGlnProGluLeuArgThrLeuGluGlySerSerAlaPheLeuProCysSer 40

Db 126 GTGTCCAGCCCTTGAGATTCGTACCTGGAAGATCTCTGCTCTCCCTCGTCTCC 185

Qy 41 PheAenAlaSerGlnGlyArgLeuAlaIleGlySerValThrTrpPheArgAspGluVal 60

Db 186 TTCAATGCCAGCAAGGAGAGACTGGCCATTGGCTCCGTCACGTGGTCCGAGATGAGGTG 245

Qy 61 ValProGlyLysGluValArgAsnGlyThrProGluPheArgGlyArgLeuAlaProLeu 80

Db 246 GTTCCAGGGAAGGAGGTGAGGAATGGAAACCCACAGATTTCAG-GGGCGGCTGGCCCCACTT 304

Qy 81 AlaSerSerArgPheLeuHisAspHisGlnAlaGluLeuHisIleArgAspValArgGly 100

Db 305 GCTTCTTCCCGTTTCTCCATGACCAACAGGCTGAGCTGCACATCCGGAGCTGGAGGC 364

Qy 101 HisAspAlaSerIleTyrValCysArgValGluValLeuGlyLeuGlyValGlyThrGly 120

Db 365 CATGACGCCAGCATCTACGTGTGCAGAGTGGAGGTGGTGGGCTTGGTGTGGGACAGGG 424

Qy 121 AsnGlyThrArgLeuValValGluLysGluHisProGlnLeuGlyAlaGlyThrValLeu 140

Db 425 AATGGGACTCGGCTGGTGGTGGAGAAAGAAATCTCTAGCTAGGGGCTGGTACAGTCTCTC 484

Qy 141 LeuLeuArgAlaGlyPheTyrAlaValSerPheLeuSerValAlaValGlySerThrVal 160

Db 485 CTCCTTCGGGCTGGATTCTATGCTGTGCTGAGCTTCTCTCTGTGGCGGTGGGAGCACCCTC 544

Qy 161 TyrTyrGlnGlyLysCysLeuThrThrTrpLysGlyProArgArgGlnLeuProAlaValVal 180

Db 545 TATTACCAGGGGCAATGTCTGACCTGGAAAGGTCCAAGAGGCAGCTGCCGGCTGTGTGTC 604

Qy 181 ProAlaProLeuProProProCysGlySerSerAlaHisLeuLeuLeuProProValProGly 200

Db 605 CCAGCGGCGCTCCACCACCATGTGGAGAGTGGAGGCTCAGCACATCTGCTTCCGCCAGTCCCAGGA 664

Qy 201 Gly 201

Db 665 GGC 667

RESULT 6

ADY16597

ID ADY16597 standard; DNA; 1116 BP.

XX AC ADY16597;

DT 05-MAY-2005 (first entry)

XX DNA encoding a PRO polypeptide, SEQ ID NO 2403.

XX Antiinflammatory; Immune disorder; Dermatological; Immunosuppressive;

XX Antirheumatic; Antiarthritic; Osteopathic; Hemostatic; Antianemic;

XX Antithyroid; Antidiabetic; Nephrotropic; CNS-Gen.; Hepatotrophic;

XX Virucide; Gastrointestinal-Gen.; Antipsoriatic; Antiasthmatic;

XX Antiallergic; de; gene; diagnosis.

XX Homo sapiens.

XX WO2005016962-A2.

XX 24-FEB-2005.

XX 11-AUG-2004; 2004WO-US026249.

XX 11-AUG-2003; 2003US-0493546P.

XX (GETH) GENENTECH INC.

XX Abbas A, Clark H, Ouyang W, Williams MP, Wood WI, Wu TD;

XX WPI; 2005-182330/19.

XX New nucleic acid encoding PRO polypeptide, useful for diagnosing and

XX treating an immune related disorder, e.g. systemic lupus erythematosus,

XX rheumatoid arthritis, osteoarthritis, thyroiditis, or diabetes mellitus.

XX Claim 1; SEQ ID NO 2403; 158pp; English.

```
XX CC The invention relates to an isolated nucleic acid encoding a PRO
CC polypeptide. The polypeptide, agonist or an antagonist, antibody,
CC composition, and method are useful for diagnosing and treating an immune
CC related disorder, e.g. systemic lupus erythematosus, rheumatoid
CC arthritis. The present sequence represents a DNA encoding a PRO
CC polypeptide.
XX SQ Sequence 1116 BP; 224 A; 343 C; 293 G; 256 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 2,49e-81 Length: 1116
Score: 1025.00 Matches: 200
Percent Similarity: 90.9% Conservative: 0
Best Local Similarity: 90.9% Mismatches: 1
Query Match: 96.1% Indels: 19
DB: 14 Gaps: 1

US-10-696-259-6 (1-201) x ADY16597 (1-1116)
Qy 1 MetAlaTrpMetLeuLeuLeuLeuLeuLeuMetValHisProGlySerCysAlaLeuTrp 20
Db 265 ATGGCCTGGATGCTGTGCTCATCTTGATCATGTCATCCAGGATCCTGTGCTCTCTGG 324
Qy 21 ValSerGlnProProGluLeuLeuArgThrLeuGluGlySerSerAlaPheLeuProCysSer 40
Db 325 GTGTCACAGCCCCCTGAGATTGCGTACCTGGAAGATCCTCTGCTTCTGCTGCTGCTCC 384
Qy 41 PheAsnAlaSerGlnGlyArgLeuAlaLeuLeuGlySerValThrTrpPheArgAspGluVal 60
Db 385 TTCAATGCCAGCCAAAGGAGAGCTGCCATTGGCTCCGTCACGTGTTCCGAGATGAGGTG 444
Qy 61 ValProGlyLysGluValArgAsnGlyThrProGluPheArgGlyArgLeuAlaProLeu 80
Db 445 GTTCACAGGAAGGAGGTGAGAAATGGAAACCCAGAGTTTCAGGGCGCGCTCGCCCACTT 504
Qy 81 AlaSerSerArgPheLeuHisAspHisGlnAlaGluLeuHisLeuArgAspValArgGly 100
Db 505 GCTTCTTCCCTTCTTCCATGACCCAGAGCTGAGCTGCACATCCGGGAGCTGGAGGC 564
Qy 101 HisAspAlaSerIleTyrValCysArgValGluValLeuGlyLeuGlyValGlyThrGly 120
Db 565 CATGAGCCAGCATCTACGTGTGCAGAGTGGAGGTGCTGGGCTTGGTGTGCGGACAGGG 624
Qy 121 AsnGlyThrArgLeuValValGluLysGluHisProGlnLeuGlyAlaGlyThrValLeu 140
Db 625 AATGGACTCGCTGTGTGTGAGAAAGAAACATCCTCAGCTAGGGGCTGGTACAGTCTCTC 684
Qy 141 LeuLeuArgAlaGlyPheTyrAlaValSerPheLeuSerValAlaValGlySerThrVal 160
Db 695 CTCCTTCGGGCTGGATTCTATGCTGTGCTGCTTCTCTCTGTGGCGGCGGAGCACCGTC 744
Qy 161 TyrTyrGlnGlyLys-Cys----- 166
Db 745 TATTACAGGCAATATATGCCAAATCTACTCTCCGGATTCCCCCAACTCTGAACCTTC 804
Qy 167 -----LeuThrTrpLysGlyProArgArgGlnLeuProAlaValProAl 182
Db 805 CTTTCCACAGCTCTGACCTGGAAGGTCCAGAAAGGAGCGCTGCCGGCTGGTGTGCTCCAGC 864
Qy 182 aProLeuProProCysGlySerSerAlaHisLeuLeuProProValProGlyGly 201
Db 865 GCCCTTCCACCAACCATGTGGAGCTCAGCATCTGCTTCTTCCCGAGTCCCGAGGAGGC 922

RESULT 7
ID AAX59348
XX AAX59348 standard; cDNA; 889 BP.
AC AAX59348;
XX XX
XX DT 20-SEP-1999 (first entry)
XX XX
XX DE Human B-cell myelin oligodendrocyte glycoprotein BMOG cDNA.
```

```
XX KW BMOG: B-cell myelin oligodendrocyte glycoprotein; human;
KW signal transduction; immunomodulator; antiinflammatory;
KW autoimmune disease; inflammation; gene therapy; diagnosis; ss.
XX OS Homo sapiens.
XX PH Location/Qualifiers
XX FT 66..598
XX CDS /*tag= a
FT /transl_except= (pos:291..292, aa:Arg)
FT /notes="this codon contains an apparent 1 nucleotide
FT deletion, which alters the reading frame"
FT sig_peptide 66..101
FT /*tag= b
FT mat_peptide 102..595
FT /*tag= c
XX XX
XX PN WO9923867-A2.
XX XX
XX PD 20-MAY-1999.
XX XX
XX PF 05-NOV-1998; 98WO-US023826.
XX XX
XX PR 07-NOV-1997; 97US-0064761P.
XX XX
XX PA (BIOJ ) BIOGEN INC.
XX XX
XX PI Browning J;
XX XX
XX WPI; 1999-418423/35.
XX DR P-PSDB; AAY06402.
XX XX
XX PT Novel B-cell myelin oligodendrocyte glycoproteins.
XX XX
XX PS Claim 1; Page 41; 43pp; English.
XX XX
XX CC This DNA sequence encodes human BMOG, a novel member of the B cell myelin
XX oligodendrocyte glycoprotein family that is expressed by germinal centre
XX B cells. 3 C-terminal splice variants (see AAY06401-03) of BMOG were
XX identified. The protein is present primarily in the spleen, in lymph
XX nodes and in germinal centre B cells. It may have immunoregulatory
XX functions, and soluble or chimeric fusion proteins of BMOG may be used to
XX regulate the immune system in autoimmune or inflammatory disease. Vectors
XX comprising BMOG, prokaryotic and eukaryotic host cells, and a method of
XX producing BMOG using these transformed host cells are also provided. BMOG
XX polypeptides can be used for modulating the immune system of a subject or
XX to inhibit signal transduction in a cell expressing BMOG by contacting it
XX with a soluble BMOG protein. The nucleic acid can be used for gene
XX therapy. The protein can also be used to target a toxin, imaging agent or
XX radionuclide to a cell expressing BMOG. (All claimed)
XX SQ Sequence 889 BP; 164 A; 281 C; 237 G; 207 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 5.72e-79 Length: 889
Score: 997.00 Matches: 199
Percent Similarity: 90.5% Conservative: 0
Best Local Similarity: 90.5% Mismatches: 2
Query Match: 93.4% Indels: 20
DB: 2 Gaps: 1

US-10-696-259-6 (1-201) x AAX59348 (1-889)
Qy 1 MetAlaTrpMetLeuLeuLeuLeuLeuMetValHisProGlySerCysAlaLeuTrp 20
Db 66 ATGGCCTGGATGCTGTGCTCATCTTGATCATGTCATCCAGGATCCTGTGCTCTCTGG 125
Qy 21 ValSerGlnProProGluLeuLeuArgThrLeuGluGlySerSerAlaPheLeuProCysSer 40
Db 126 GTGTCACAGCCCCCTGAGATTGCGTACCTGGAAGATCCTCTGCTTCTGCTGCTGCTCC 185
Qy 41 PheAsnAlaSerGlnGlyArgLeuAlaLeuLeuGlySerValThrTrpPheArgAspGluVal 60
```

Db 186 TTCATGCGACCGAAGGAGACTGGCCATTGGCTCCGTCACGTGGTTCGAGATGAGGTG 245
Qy 61 ValProGlyLysGluValArgAsnGlyThrProGluPheArgGlyValGluAlaProLeu 80
Db 246 GTTCAGGGAAGGAGTGGAGTGAATGAAACCCAGAGTTCAG-GGGCGCTGGCCCACTT 304
Qy 81 AlaSerSerArgPheLeuHisAspHisGlnAlaGluLeuHisIleArgAspValArgGly 100
Db 305 GCTTCTTCCTCCGTTTCTCCATGACCCAGGCTGAGCTGCACATCCGGGAGCTGGAGGC 364
Qy 101 HisAspAlaSerIleTyrValCysArgValGluValLeuGlyValGlyThrGly 120
Db 365 CATGACGCCAGCACTACGTGTGCAGAGTGGAGGCTGGGGCTTGGTGTGGGACAGG 424
Qy 121 AsnGlyThrArgLeuValValGluLysGluHisProGlnLeuGlyValAlaGlyThrValLeu 140
Db 425 AATGGACTCGCTGGTGGTGGAGAAAGAAACATCTCAGCTAGGGCTGGTACAGTCTCTC 484
Qy 141 LeuLeuArgAlaGlyPheTyrAlaValSerPheLeuSerValAlaValGlySerThrVal 160
Db 485 CTCCTTCGGGTGGATTCTATGTGTCTGCTGCTCTCTCTGTGGCGTGGCGAGCACCCTC 544
Qy 161 TyrTyrGlnGlyLys-Cys----- 166
Db 545 TATTACCGAGGCAATATGCCAAATCTACTCTCCGATTCCTCCCAACTCTGAACTTTC 604
Qy 167 -----LeuThrTyrLysGlyProArgArgGlnLeuProAlaValProAl 182
Db 605 CCTTCCACCGTCTGACTCGAAGGTCGAAGAGGAGTGGCGGCTGTGTTCCAGC 664
Qy 182 aProLeuProProCysGlySerSerAlaHisLeuLeuProProValProGlyGly 201
Db 665 GCCCTCCACCAACCATGTGGAGCTCAGCACATCTGCTTCCCCCAGTCCCAGGAGGC 722

RESULT 8

AD019809
ID AD019809 standard; cDNA; 573 BP.
XX
AC AD019809;
XX
DT 12-AUG-2004 (first entry)
XX
DE Human PRO polynucleotide #367.
XX
KW Human; PRO; gene; ss; immune related disorder;
KW systemic lupus erythematosus; rheumatoid arthritis; osteoarthritis;
KW juvenile chronic arthritis; systemic sclerosis; Sjogren's syndrome;
KW vasculitis; sarcoidosis; autoimmune haemolytic anaemia;
KW autoimmune thrombocytopenia; thyroiditis; diabetes mellitus;
KW renal disease; demyelinating disease; central nervous system;
KW peripheral nervous system; demyelinating polyneuropathy;
KW Guillain-Barre syndrome;
KW chronic inflammatory demyelinating polyneuropathy.
XX
OS Homo sapiens.
XX
FN WO2004043361-A2.
XX
PD 27-MAY-2004.
XX
PF 06-NOV-2003; 2003WO-US035268.
XX
PR 08-NOV-2002; 2002US-0425235P.
XX
PA (GETH) GENENTECH INC.
XX
PI Fong S, Dennis K, Clark H, Chiu H, Schoenfeld J, Williams PM;
PI Wood WI, Wu TD;
XX
DR WPI: 2004-420067/39.
DR P-PSDB; AD019810.
XX

PT Novel PRO polypeptide e.g., PRO69614, PRO71106, or PRO86388 useful for
PT treating an immune related disorder such as systemic lupus erythematosus,
PT rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis or
PT spondyloarthritis.
XX
PS Claim 1; SEQ ID NO 758; 1731pp; English.
XX

CC The invention relates to human PRO polypeptides and the polynucleotides
CC encoding them. The polypeptides and polynucleotides are useful for
CC treating and diagnosing immune related disorders in mammals. The immune
CC related disorders include systemic lupus erythematosus, rheumatoid
CC arthritis, osteoarthritis, juvenile chronic arthritis, systemic
CC sclerosis, Sjogren's syndrome, vasculitis, sarcoidosis, autoimmune
CC haemolytic anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes
CC mellitus, immune-mediated renal disease, demyelinating diseases of the
CC central or peripheral nervous system, demyelinating polyneuropathy,
CC Guillain-Barre syndrome and chronic inflammatory demyelinating
CC polyneuropathy. This sequence represents a human PRO polynucleotide of
CC the invention.

SQ Sequence 573 BP; 101 A; 168 C; 173 G; 130 T; 0 U; 1 Other;

Alignment Scores:

Pred. No.: 1.76e-68 Length: 573
Score: 876.00 Matches: 173
Percent Similarity: 90.2% Conservative: 2
Best Local Similarity: 89.2% Mismatches: 7
Query Match: 82.1% Indels: 12
DB: 12 Gaps: 2

US-10-696-259-6 (1-201) x AD019809 (1-573)

Qy 1 MetAlaTrpMetLeuLeuLeuLeuMetValHisProGlySerCysAlaLeuTrp 20
Db 1 ATGCGCTGGATGCTGTGCTCATCTTCATCATGTTCATCCAGATCTCTGTCTCTGG 60
Qy 21 ValSerGlnProProGluLeuArgThrLeuGluGlySerSerAlaPheLeuProCysSer 40
Db 61 GTGTCCAGGCCCTCTGAGATTCGTACCTTGAAGGATCTCTGCTCTCTGCTCTCTCC 120
Qy 41 PheAsnAlaSerGlnGlyArgLeuAlaIleGlySerValThrPheArgAspGluVal 60
Db 121 TTCAATGCCAGCCAGGAGAGTGGCAATGGAAATGGATTCAGCTGGTTCGAGATGAGGTG 180
Qy 61 ValProGlyLysGluValArgAsnGlyThrProGluPheArgGlyValGluAlaProLeu 80
Db 181 GTTCAGGGAAGGAGGTGAGGAATGGAAATGGATTCAGGAGGCGCTGGCCCACTT 240
Qy 81 AlaSerSerArgPheLeuHisAspHisGlnAlaGluLeuHisIleArgAspValArgGly 100
Db 241 GCTTCTTCCTGTTTCTCCATGACCAAGGCTGAGTGCACATCCGGGAGCTGGAGGC 300
Qy 101 HisAspAlaSerIleTyrValCysArgValGluValLeuGlyValGlyThrGly 120
Db 301 CATGACGCCAGCATCTACGTGTGCAGAGTGGAGTGTGGGCTTGGTGTGGGACAGG 360
Qy 121 AsnGlyThrArgLeuValGluLysGluHisProGlnLeuGlyValGlyThrValLeu 140
Db 361 AATGGACTCGCTGGTGGTGGAGAAAGAACATCTCAGTAGGGGCTGGTACAGTCTCTC 420
Qy 141 LeuLeuArgAlaGlyPheTyrAlaValSerPheLeuSerValAlaValGlySerThrVal 160
Db 421 CTCCTTCGGGCTGGATTCTATGTGTCTCAGCTTTCTCTGTGGCGCTGGGAGCAGCCTC 480
Qy 161 TyrTyrGlnGlyLys-----CysLeuThrTrpLysGlyPro 172
Db 481 TATTACCGAGGCAATATGCCACTGTACATGGGAACACACTGCCACTCTCAGATGGGCCC 540
Qy 173 ArgArgGlnLeuProAlaValValProAlaProLeuProPro 186
Db 541 CGA-----GGGTGATTCAGAGCCAGCCAGATGTCTCC 570

RESULT 9

XX PF 15-NOV-2000; 2000WO-EP011697.
 XX PR 15-NOV-1999; 99CA-02288307.
 XX PR 15-NOV-1999; 99US-00440514.
 XX PA (INNA-) INNATE PHARMA SAS.
 XX PA (UYGE-) UNIV GENOVA.
 XX FI Moretta A, Bottino C, Biassoni R;
 XX DR WPI; 2001-329221/34.
 XX DR P-PSDB; AAE02769.
 XX PT Novel compound, useful for detection and/or quantifying the presence of
 XX PT NK cells, comprises the amino acid sequences of the NKp30 molecule.
 XX PS Claim 3; Page 59; 83pp; English.
 XX CC The invention relates to human NKp30 receptor and its corresponding cDNA
 XX CC molecule which is involved in natural cytotoxicity mediated by natural
 XX CC killer (NK) cells and antibodies that identify the same. NKp30 receptor
 XX CC is a member of immunoglobulin super family (Ig-SF). NKp30 is selectively
 XX CC expressed on the surface of human mature NK cells. NKp30 and its cDNA are
 XX CC useful for detecting and/or quantifying the presence of NK cells in a
 XX CC biological sample. The invention also provide kits for detecting and/or
 XX CC quantifying the presence of NK cells, for the selective removal of NK
 XX CC cells from a biological sample, for the positive and selective
 XX CC purification of NK cells from a biological sample and for the in vitro
 XX CC stimulation of NK cell cytotoxicity. The invention further provides a
 XX CC pharmaceutical composition which is used as a drug for grafting
 XX CC enhancement, graft versus host (GVH) inhibition, stimulation of graft
 XX CC versus tumour (GVT) and especially graft versus leukaemia (GVL), and for
 XX CC the prevention, palliation and/or therapy of solid or liquid tumours,
 XX CC such as melanoma, hepatocarcinoma and lung adenocarcinoma, and/or
 XX CC microorganism, notably viral infection. NKp30 antibodies are useful for
 XX CC identifying NKp30 natural ligands and allow assessment of the level of
 XX CC surface NKp30 ligand expressed on an NK-susceptible target cell and the
 XX CC comparison of this level to the standard physiological one. Hence NKp30
 XX CC antibodies are useful in the diagnosis of tumours or of infection. The
 XX CC present cDNA sequence encodes human NKp30 receptor
 XX SQ Sequence 674 BP; 124 A; 214 C; 183 G; 152 T; 0 U; 1 Other;

Alignment Scores:
 Pred. No.: 2.15e-68 Length: 674
 Score: 876.00 Matches: 173
 Percent Similarity: 90.2% Conservative: 2
 Best Local Similarity: 89.2% Mismatches: 7
 Query Match: 82.1% Indels: 12
 DB: 4 Gaps: 2

US-10-696-259-6 (1-201) x AAD06564 (1-674)

Qy 1 MetAlaTrpMetLeuLeuLeuLeuLeuLeuMetValHisProGlySerCysAlaLeuTrp 20
 Db 64 ATGGCTGGATGCTGTCTCATCTTGATCATGTGTCATCCAGGATCTGTGCTCTCTGG 123
 Qy 21 ValSerGlnProGluIleArgThrIleuGluGlySerSerAlaPheLeuProCysSer 40
 Db 124 GTGTCCACAGCCCTCGAGATTGCTACCCCTGGAGGATCTCTGCTTCTCTGCTGCTCC 183
 Qy 41 PheAsnAlaSerGlnGlyArgLeuAlaIleGlySerValThrTrpPheArgAspGluVal 60
 Db 184 TTCATGCCACGACCAAGGAGACTGGCCATTGGCTCCGTCAGTGGTTCGAGATGAGGTG 243
 Qy 61 ValProGlyLysGluValArgAsnGlyThrProGluPheArgGlyArgLeuAlaProLeu 80
 Db 244 GTTCCAGGAAGGAGGTGAGGAATGTAACCCACAGATTACGGGCGCGCTGCGCCCACTT 303
 Qy 81 AlaSerSerArgPheLeuHisAspHisGlnAlaGluLeuHisIleArgAspValArgGly 100
 Db 304 GCTTCTTCCCGTTTCTCCATGACCAACAGGCTGAGCTGACATCCCGGACGTGCGAGGC 363

Qy 101 HisAspAlaSerIleTyrValCysArgValGluValLeuGlyLeuGlyValGlyThrGly 120
 Db 364 CATGACGCCAGCATCTACGTGTGCAGAGTGGAGGTGCTGGGCCCTTGGTGTGGACACGGG 423
 Qy 121 AsnGlyThrArgLeuValValGluLysGluHisProGlnLeuGlyAlaGlyThrValLeu 140
 Db 424 AATGGGACTCGGCTGGTGGTGGAGAAAGAACATCTCAGCTAGGCTAGGGGTGGTACAGTCCTC 483
 Qy 141 LeuLeuArgAlaGlyPheTyrAlaValSerPheLeuSerValAlaValGlySerThrVal 160
 Db 484 CTCCTTCGGGCTGGATTCTATGCTGTCTCTCTGTGGCGGTGGGAGGACCCGTC 543
 Qy 161 TyrTyrGlnGlyLys-----CysLeuThrTrpLysGlyPro 172
 Db 544 TATTACAGGGCAATGCCACTGTCACATGGGAACACACTGCCACTCTCAGATGGGCC 603
 Qy 173 ArgArgGlnLeuProAlaValValProAlaProLeuProPro 186
 Db 604 CGA-----GGRGTGATTCCAGAGCCAGATGTCCC 633
 RESULT 11
 ADQ59392
 ID ADQ59392 standard; DNA; 22173 BP.
 AC ADQ59392;
 XX 07-OCT-2004 (first entry)
 DT Human cancer-associated (CA) gene sequence SEQ ID NO:28.
 DE human; cancer-associated gene; cancer-associated protein; cytostatic;
 KW gene therapy; vaccine; tyrosine kinase antagonist;
 KW G-protein coupled receptor antagonist; cancer; lymphoma; gene; ds.
 XX Homo sapiens.
 OS WO2004058288-A1.
 XX 15-JUL-2004.
 PD 15-DEC-2003; 2003WO-US040082.
 PF 17-DEC-2002; 2002US-00322696.
 XX (SAGR-) SAGRES DISCOVERY INC.
 PA Morris DW, Malandro MS;
 XX WPI; 2004-543349/52.
 DR P-PSDB; ADQ59394.
 XX New cancer-associated nucleic acid for diagnosing, preventing or treating
 PT cancer (e.g. lymphoma) or for screening agents that may be used for
 PT treating or preventing cancer.
 XX Claim 16; SEQ ID NO 28; 143pp; English.
 XX The present invention describes human cancer-associated (CA) nucleotide
 CC sequences (1). Also described: (1) an expression vector comprising (1);
 CC (2) a host cell comprising (1) or the expression vector; (3) a microarray
 CC for detecting a CA nucleic acid; (4) an isolated polypeptide encoded
 CC within an open reading frame of a CA sequence; (5) an isolated antibody,
 CC or its antigen binding fragment, that binds to the above polypeptide; (6)
 CC a hybridoma that produces the monoclonal antibody described above; (7) a
 CC pharmaceutical composition comprising the antibody and a pharmaceutical
 CC excipient; (8) a kit for detecting or diagnosing cancer cells, comprising
 CC the above (monoclonal) antibody or polynucleotide that selectively
 CC hybridises to any of the polynucleotide sequences mentioned above; (9)
 CC methods for diagnosing cancer or for detecting the presence or absence of
 CC cancer cells in an individual; (10) a method for inhibiting growth of
 CC cancer cells in an individual; (11) a method for delivering a therapeutic
 CC agent to cancer cells in an individual; (12) an electronic library

CC	comprising the polynucleotide or polypeptide, or their fragments;	
CC	mentioned above; (13) a method of screening for anticancer activity; (14)	
CC	methods for detecting cancer associated with expression of a polypeptide	
CC	or the presence of the antibody in a test cell or serum sample; (15) a	
CC	method for screening for a bioactive agent capable of modulating the	
CC	activity of a CA protein encoded by the above nucleic acid molecule; and	
CC	(16) a method for treating cancers. (1) has cytostatic activity, and can	
CC	be used in gene therapy, in vaccines, as a tyrosine kinase antagonist,	
CC	and as a G-protein coupled receptor antagonist. The compositions and	
CC	methods of the present invention can be used for diagnosing, preventing	
CC	and treating cancer, especially lymphomas. They may also be used in	
CC	screening for agents that may be used for treating or preventing cancer.	
CC	The present sequence represents a human CA gene sequence, which is given	
CC	in the exemplification of the present invention. Note: The sequence data	
CC	for this patent did not form part of the printed specification, but was	
CC	obtained in electronic format directly from WIPO at	
CC	ftp.wipo.int/pub/published_pct_sequences.	
XX		
SQ	Sequence 22173 BP; 4786 A; 5863 C; 5847 G; 5677 T; 0 U; 0 Other;	
Alignment Scores:		
Pred. No.:	3.36e-66	Length: 22173
Score:	872.00	Matches: 191
Percent Similarity:	52.5%	Conservative: 1
Best Local Similarity:	52.2%	Mismatches: 2
Query Match:	81.7%	Indels: 172
DB:	12	Gaps: 3
US-10-696-259-6 (1-201) x ADQ59392 (1-22173)		
QY	3 TrpMetLeuLeuLeuLeuLeuMetValHisProGlySerCysAlaLeuTyrValSer 22	
DB	2577 TGGGTCTTCCTCTG-----CCCCCAGGATCCTGGCTCTCTGGGTGCC 2621	
QY	23 GlnProGluIleArgThrLeuGluGlySerSerAlaPheLeuProCysSerPheAsn 42	
DB	2622 CAGCCCCCTGAGATTCGTACCTCGAAGGATCCTCTGCTTCTGCTGCTCTCAAT 2681	
QY	43 AlaSerGlnGlyArgLeuAlaIleGlySerValThrTrpPheArgAspGluValValPro 62	
DB	2682 GCCACCAAGGAGAGTGGCCATTGGCTCCGTCACGTGGTTCGAGATGAGTGGTCCA 2741	
QY	63 GlyLysGluValArgAsnGlyThrProGluPheArgGlyArgLeuAlaProLeuAlaSer 82	
DB	2742 GGGAAAGGAGTGAGGAATGGAAACCCACAGATTACGGGCGCGCTGGCCCCACTGCTTCT 2801	
QY	83 SerArgPheLeuHisAspHisGlnAlaGluLeuHisIleArgAspValArgGlyHisasp 102	
DB	2802 TCCCGTTTCTTCATGACCCACAGCTGAGCTGCACATCCGGGACGTGCGAGGCCATGAC 2861	
QY	103 AlaSerIleTyrValCysArgValGluValLeuGlyValGlyValGlyThrGlyAsnGly 122	
DB	2862 GCCAGCATCTAGCTGTCAGAGTGGAGGTGCTGGGCCCTTGGTGTGGGACAGGAATGG 2921	
QY	123 ThrArgLeuValValGlu-Lys----- 129	
DB	2922 ACTCGGCTGGTGGTGGAAAGGTGAGATGCTGGGAGGTGGTGTCTCTCTGGCTGGAG 2981	
QY	129 ----- 129	
DB	2982 GCCCCAAGAGCAATGTCCTTGGGAGGCGAGGATGCTCCTCTGAGGCCCTTCCCTCCCT 3041	
QY	130 -----GluHisProGln 133	
DB	3042 GAGCCTGTGTGACTTCTTCCCAACCCCGTCTCCATTGGCCCCCATGGAGACATCTCTCA 3101	
QY	133 nLeuGlyAlaGlyThrValLeuLeuLeuArgAlaGlyPheTyrAlaValSerPheLeuSe 153	
DB	3102 GCTAGGGGCTGGTACAGTCTCTCTCTGGGCTGGATTCTATGCTGTGAGTCTCTCTC 3161	
QY	153 rValAlaValGlySerThrValTyrTyrGlnGlyLysCys----- 166	
DB	3162 TGTGGCGTGGGAGCACCGCTCTATTACCAGGGGCAATGTGAGTAATGGAGCCAGGGGCA 3221	

QY	166 ----- 166	
DB	3222 ATAGTGGACGGATGGGAGGGGCACGTAAAGAGTGGGAGGAGGAGACAGAGACAGGA 3281	
QY	166 ----- 166	
DB	3282 AGAGGAGAGCCTCGGACGTGCAACACTGAGCAGCTCTGTCTCTCTGTGACCGGCCAC 3341	
QY	166 ----- 166	
DB	3342 TGTACATGGGAACACACTGCCACTCCTCAGATGGGCCCCGAGGAGTGTATCCAGAGCCC 3401	
QY	166 ----- 166	
DB	3402 AGATGTCCCTAGTCTCTTCAAAGACCCCAATAAATCTGCCCCACCACTAACTCTCAT 3461	
QY	166 ----- 166	
DB	3462 GAGTCTCAAGTGTCTTCTTCTCCATTCTCCAGATGCCAAATCTACTCTCTCCGATTCCC 3521	
QY	167 -----LeuThrTrpLysGlyProArgArgGlnLeuP 177	
DB	3522 CCAACTCTGAACCTTCCCTTCCACAGGTCTGACCTGGAAAGGTCCAGAGAGGCAGCTGC 3581	
QY	177 roAlaValValProAlaProLeuProProCysGlySerSerAlaHisLeuLeuProp 197	
DB	3582 CGGTGTGGTCCCGAGCGCCCTCCACACCATGTGGGAGCTCAGCACATCTGCTTCCCC 3641	
QY	197 roValProGlyGly 201	
DB	3642 CAGTCCCGAGGAGGC 3655	
RESULT 12		
ADZ13655	ADZ13655 standard; DNA; 22173 BP.	
XX	ADZ13655	
AC	ADZ13655;	
XX	16-JUN-2005 (first entry)	
DT	Human cancer-associated genomic DNA #101.	
DE		
XX	Diagnosis; DNA microarray; microarray; biochip; cancer; neoplasm;	
KW	cytostatic; gene; ds.	
XX	Homo sapiens.	
OS	WO2005031001-A2.	
XX	07-APR-2005.	
PD	23-SEP-2004; 2004WO-US031617.	
PF	23-SEP-2003; 2003US-00669920.	
XX	(CHIR) CHIRON CORP.	
PA	Morris DW, Malandro MS;	
XX	WPI; 2005-273395/28.	
DR	Nucleic acid array useful for detecting cancer associated nucleic acid,	
PT	comprises two or more nucleic acid probes.	
XX	Disclosure; SEQ ID NO 1175; 198pp; English.	
PS	The invention relates to a nucleic acid array for detecting a cancer	
CC	associated (CA) nucleic acid, comprising two or more nucleic acid probes.	
CC	The invention also relates to a peptide array comprising two or more	
CC	isolated polypeptides encoded by a CA nucleic acid sequence, a compound	
CC	that binds to a polypeptide, an isolated antibody or its fragment which	
CC	binds to a polypeptide, which is prepared by immunizing a host animal	

CC with a composition comprising the polypeptide or its antigen binding
 CC fragment and collecting cells from the host expressing antibodies against
 CC the antigen or its antigen binding fragment, a composition comprising the
 CC antibody and a carrier, a method of screening for anticancer activity, a
 CC method of detecting a CA nucleic acid, a method of diagnosing cancer, a
 CC method of treating cancer and a method of inhibiting expression of a CA
 CC nucleic acid in a cell. The CA nucleic acids are useful for detecting CA
 CC nucleic acids. The antibody is useful for detecting the presence or
 CC absence of cancer cells in an individual which involves contacting cells
 CC from the individual with the antibody and detecting a complex of a CA
 CC protein from the cancer cells and the antibody, where the detection of
 CC the complex correlates with the presence of cancer cells in the
 CC individual. The composition is useful for inhibiting growth of cancer
 CC cells in an individual or for delivering a therapeutic agent to cancer
 CC cells in an individual. The invention is also useful for diagnosing
 CC cancer, for treating cancer and for inhibiting expression of a CA gene in
 CC a cell. This sequence represents human cancer-associated genomic DNA of
 CC the invention.

SQ Sequence 22173 BP; 4785 A; 5863 C; 5847 G; 5678 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 3.36e-66 Length: 22173
 Score: 872.00 Matches: 191
 Percent Similarity: 52.5% Conservative: 1
 Best Local Similarity: 52.5% Mismatches: 2
 Query Match: 81.7% Indels: 172
 DB: 14 Gaps: 3

US-10-696-259-6 (1-201) x ADZ13655 (1-22173)

Qy 3 TrpMetLeuLeuLeuLeuLeuMetValHisProGlySerCysAlaLeuTrpValSer 22
 Db 2577 TGGGTCTTCTTCG-----CCCCCAGGATCCTGTGCTCTCTGGGTGCC 2621
 Qy 23 GluProGluLeuArgThrLeuGluGlySerSerAlaPheLeuProCysSerPheAsn 42
 Db 2622 CAGCCCCCTGAGATTCGTACCTCGAAGGATCCTCTGCTTCTTGGCCCTGCTCCTCAAT 2681
 Qy 43 AlaSerGlnGlyArgLeuAlaIleGlySerValThrTrpPheArgAspGluValValPro 62
 Db 2682 GCCAGCCAGGAGACTGGCCATTGGCTCCGTACGTGGTTCAGATGAGGTGGTTCCA 2741
 Qy 63 GlyLysGluValArgAsnGlyThrProGluPheArgGlyArgLeuAlaProLeuAlaSer 82
 Db 2742 GGGAAAGAGGTGAGGAATGGAACCCAGAGTTTCAGGGCGCCCTGGCCCTTGTCTTCT 2801
 Qy 83 SerArgPheLeuHisAspHisGlnAlaGluLeuHisIleArgAspValArgGlyHisAsp 102
 Db 2802 TCCCGTTTCTCTCCATGCCACAGGCTGAGCTGCACATCCGGGACGTGCGAGGCCATGAC 2861
 Qy 103 AlaSerIleTyrValCysArgValGluValLeuGlyValGlyThrGlyAsnGly 122
 Db 2862 GCCAGCATCTACGTGTGCAGATGAGGTGCTGGGCCCTTGTGTGCGGACAGGGAATGGG 2921
 Qy 123 ThrArgLeuValValGlu-Lys----- 129
 Db 2922 ACTCGGTGGTGGTGGAAAGGTGAGATGTGGGAGGTGGTGTCTCTCTCTGCTGGAG 2981
 Qy 129 ----- 129
 Db 2982 GCCCAAGAGGCAATGTCTTTGGGAGGCGAGGATGCTCCTCTGAGGCCCTTCCCTCCCT 3041
 Qy 130 -----GluHisProG1 133
 Db 3042 GAGCTGTGTGCACTTCTTCCCCAACCCCGTCTCCATTTGCCCATCGAACAATCTCA 3101
 Qy 133 nLeuGlyAlaGlyThrValLeuLeuLeuArgAlaGlyPheTyrAlaValSerPheLeuSe 153
 Db 3102 GCTAGGGCTGGTACAGTCTCTCTCTTGGGCTGGATTCTATGCTGTCTGAGTTTCTCTC 3161
 Qy 153 rValAlaValGlySerThrValTyrTyrGlnGlyLysCys----- 166
 |||||||

Db 3162 TGTGGCCGTGGGCGAGCACCGTCTATTACCAGGGCAAAATGTGAGTAATGGAGCCAGGGGCA 3221
 Qy 166 ----- 166
 Db 3222 ATAGTGACCGGATGGGAGGGCGAGTAGAGAGATGGGAGGAGGAGGACAGAGACCAGGA 3281
 Qy 166 ----- 166
 Db 3282 AGAGGAGAGCCTCGGAGACTGCAACACTGAGCAGCTCCTGTCTCTCTGTGACCAGGCCAC 3341
 Qy 166 ----- 166
 Db 3342 TGTCACATGGGAACACACTGCCACTCTCCTCAGATGGGCCCCCGAGAGTGATTTCCAGAGCCC 3401
 Qy 166 ----- 166
 Db 3402 AGATGTCCCTAGTCTCTTCAAAAGACCCCAATAAATCTGCCCCCACCACCTAACTCTCAT 3461
 Qy 166 ----- 166
 Db 3462 GAGTCTCAAGTGTCTTCTCTCCATTCTCCAGATGCCAAATCTACTCTCCGGATTCCC 3521
 Qy 167 -----LeuThrTTrpLysGlyProArgArgGlnLeuP 177
 Db 3522 CCAACTCTGAACCTTTCCTTCCACAGGTCTGACCTGGAAGGTCCAAAGAGGAGCTGC 3581
 Qy 177 roAlaValValProAlaProLeuProProCysGlySerSerAlaHisLeuLeuProP 197
 Db 3582 CGGCTGTGTCTCCAGGCGCCCTCCACCACCATGTGGAGCTCAGCACATCTGCTTCCCC 3641
 Qy 197 roValProGlyGly 201
 Db 3642 CAGTCCAGGAGGC 3655
 RESULT 13
 ABK84756
 ID ABK84756 standard; cDNA; 81800 BP.
 XX
 AC ABK84756;
 XX
 DT 14-AUG-2002 (first entry)
 XX
 DE Human cDNA differentially expressed in granulocytic cells #1327.
 XX
 KW Human; ss; granulocytic cell; DNA chip; bacterial infection;
 KW viral infection; parasitic infection; protozoal infection;
 KW fungal infection; sterile inflammatory disease; psoriasis;
 KW rheumatoid arthritis; glomerulonephritis; asthma; thrombosis;
 KW cardiac reperfusion injury; renal reperfusion injury; ARDS;
 KW adult respiratory distress syndrome; inflammatory bowel disease;
 KW Crohn's disease; ulcerative colitis; periodontal disease;
 KW granulocyte activation; chronic inflammation; allergy.
 XX
 OS Homo sapiens.
 XX
 XX WO200228999-A2.
 XX
 XX 11-APR-2002.
 XX
 PF 03-OCT-2001; 2001WO-US030821.
 XX
 PR 03-OCT-2000; 2000US-0237189P.
 XX
 XX (GENE-) GENE LOGIC INC.
 XX
 XX Beazer-Barclay Y, Weissman SM, Yamaga S, Vockley J;
 XX WPI; 2002-435328/46.
 XX
 PT Detecting granulocyte activation by detecting differential expression of
 PT genes associated with granulocyte activation, which serves as diagnostic
 PT markers that is useful for monitoring disease states and drug toxicity.
 XX

```
PS Claim 1; SEQ ID NO 1327; 114pp; English.
XX
CC The invention relates to detecting (M1) granulocyte (GC) activation
CC (GCA), by detecting the level of expression of gene(s) (Gs) identified by
CC DNA chip analysis as given in the specification, and comparing the
CC expression level to an expression level in an unactivated GC, where
CC differential expression of Gs is indicative of GCA. Also included are
CC modulating (M2) GC by contacting GC with an agent that alters the
CC expression of at least one gene in Gs; (2) screening (M3) for an agent
CC capable of modulating GCA or an inflammation (especially chronic) in a
CC tissue, an allergic response in a subject, exposure of a subject to a
CC pathogen or sterile inflammatory disease using the gene expression
CC profile; (3) detecting (M4) an inflammation (especially chronic) in a
CC tissue, an allergic response in a subject, exposure of a subject to a
CC pathogen or sterile inflammatory disease, by detecting the level of
CC expression in a sample of the tissue of gene(s) from Gs, where the level
CC of expression of the gene is indicative of inflammation; (4) treating
CC (M5) an inflammation (especially chronic) or in a tissue, an allergic
CC response in a subject, exposure of a subject to a pathogen or sterile
CC inflammatory disease, by contacting a tissue having inflammation with an
CC agent that modulates the expression of gene(s) from Gs in the tissue. M1
CC is useful for detecting GCA; M2 is useful for modulating GCA; M3 is useful
CC for screening an agent capable of modulating GCA preferably in an
CC inflammation in a tissue; M4 is useful for detecting an inflammation
CC (especially chronic) in a tissue, an allergic response in a subject,
CC exposure of a subject to a pathogen or sterile inflammatory disease (e.g.
CC psoriasis, rheumatoid arthritis, glomerulonephritis, asthma, thrombosis,
CC cardiac reperfusion injury, renal reperfusion injury, ARDS, adult
CC respiratory distress syndrome, inflammatory bowel disease, Crohn's
CC disease, ulcerative colitis, periodontal disease; also bacterial
CC infection, viral infection, parasitic infection, protozoal infection,
CC fungal infection and M5 is useful for treating one of the above
CC conditions. The present sequence represents a gene differentially
CC expressed in granulocytes. Note: The sequence data for this patent did
CC not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences

SQ Sequence 81800 BP; 19886 A; 19955 C; 20623 G; 21336 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.64e-65 Length: 81800
Score: 872.00 Matches: 191
Percent Similarity: 52.5% Conservative: 1
Best Local Similarity: 52.2% Mismatches: 2
Query Match: 81.7% Indels: 172
DB: 6 Gaps: 3

US-10-696-259-6 (1-201) x ABK84756 (1-81800)

QY 3 TrpMetLeuLeuLeuLeuLeuLeuMetValHisProGlySerCysAlaLeuTrpValSer 22
DB 29464 TGGGTCTTCTCTCTG-----CCCCCAGGATCTGTGCTCTCTGGGTGTC 29508

QY 23 GlnProGluIleArgThrLeuGluGlySerSerAlaPheLeuProCysSerPheAsn 42
DB 29509 CAGCCCCCTGAGATTCTGATCTGGAAGGATCTCTGCTTCTCTGCTCTCTCTCAAT 29568

QY 43 AlaSerGlnGlyArgLeuAlaIleGlySerValThrTrpPheArgAspGluValPro 62
DB 29569 GCCAGCAAGGAGAGCTGCCATTTGGCTCCGCTCAGCTGTCATCCGGAGATGAGGTGTTCCA 29628

QY 63 GlyIleGluValArgAsnGlyThrProGluPheArgGlyArgLeuAlaProLeuAlaSer 82
DB 29629 GGGAAAGGAGGTGAGGAATGGAAACCCAGATTTCAGGGGCGGCTGGCCCCCTCTCTCT 29688

QY 83 SerArgPheLeuHisAspHisGlnAlaGluLeuHisIleArgAspValArgGlyHisAsp 102
DB 29689 TCCCGTTCTTCCATGACACACCAGCTGAGCTGACATCCGGGAGCTGCGAGGCCATGAC 29748

QY 103 AlaSerIleTyrValCysArgValGluValLeuGlyValGlyThrGlyAsnGly 122
DB 29749 GCCAGCATCTACGTGTCAGAGTGGAGGTGCTGGGCGCTTGGGTGTCGGGACAGGGAATGG 29808

QY 123 ThrArgLeuValValGlu-Lys----- 129
DB 29809 ACTCGCTGCTGCTGGAGAAAGTGTGAGATGCTGGGAGGTGGTGTCTCTCTCTCTGGCTGGAG 29868

QY 129 ----- 129
DB 29869 GCCCAAGAGGCAATGTCTCTGGGAGGAGGATGTCTCTCTGAGGCCCTTCCCTCCCT 29928

QY 130 -----GluHisProG1 133
DB 29929 GAGCCTGTGTGCACTTCTTCCCAACCCCGCTCTCCATTGCCCATGCAAGAACTCTCA 29988

QY 133 nleuGlyAlaGlyThrValLeuLeuLeuArgAlaGlyPheTyrAlaValSerPheLeuSe 153
DB 29989 GCTAGGGGCTGGTACAGTCTCTCTCTCTCGGCTGGATTCTATGTCTGTCTCTCTCTC 30048

QY 153 rValAlaValGlySerThrValTyrTyrGlnGlyLysCys----- 166
DB 30049 TGTGGCGGTGGGCGAGCACCGCTCTATTACCAGGGCAATGTGAGTAATGGAGCCAGGGGCA 30108

QY 166 ----- 166
DB 30109 ATAGTGCACGGGATGGGAGGGGCGAGTAAGAGATGGGAGGAGGAGGACAGACCAGGA 30168

QY 166 ----- 166
DB 30169 AGAGGAGAGCTCGGAGCTGCAACACTGAGCAGCTCTGTCTCTCTCTGACCAGGCCAC 30228

QY 166 ----- 166
DB 30229 TGTACATGGGAACACACTGCCACTCTCTCAGATGGGCGCCGAGGAGTGTATCCAGAGCCC 30288

QY 166 ----- 166
DB 30289 AGATGTCCCTAGTCTCTTTCAAAGAGCCCAATAAATCTGCCCCACCACTAATCTCTCAT 30348

QY 166 ----- 166
DB 30349 GAGTCTCAAGTGTCTTCTCTCTCCATCTCCAGATGCCAAATCTACTCTCTCCGATTCCC 30408

QY 167 -----LeuThrTrpLysGlyProArgArgGlnLeuP 177
DB 30409 CCAACTCTGAACCTTTCCCTTCCACAGGTCTGACCTGGAAGGTCCAAGAGGCGAGCTGC 30468

QY 177 roAlaValValProAlaProLeuProProCysGlySerSerAlaHisLeuLeuProp 197
DB 30469 CGGCTGTGTTCCCGAGCGCCCTCTCCACCAATGTGGAGCTCAGCACATCTGCTTCCCC 30528

QY 197 roValProGlyGly 201
DB 30529 CAGTCCCAGGAGGC 30542

RESULT 14
ADW38506/c
ID ADW38506 standard; cDNA; 6853 BP.
XX
AC ADW38506;
XX
XX 24-MAR-2005 (first entry)
XX
DE Immunomodulatory gene LST-1 cDNA.
XX
KW cytostatic; immunosuppressive; virucide; diagnosis; prognosis;
KW pharmaceutical; immunotherapy; cancer; cytostatic; neoplasm;
KW autoimmune disease; immunosuppressive; immune disorder; viral infection;
XX infection; LST-1; gene; ss.
XX
OS Homo sapiens.
XX
XX WO2005000099-A2.
XX
PD 06-JAN-2005.
```

XX 09-JUN-2004; 2004WO-US018461.
XX
XX
XX 09-JUN-2003; 2003US-0477291P.
XX
XX (GENZ) GENZYME CORP.
XX
XX Roberts BL;
XX
XX WPI; 2005-058046/06.
XX P-PSDB; ADW38505.
XX
XX New isolated blood factor domain polynucleotides having immunomodulatory
PT activity, useful for aiding in the diagnosis or treating disorders
PT relating to the immune responses, e.g. cancers, autoimmune diseases, or
PT viral infections.
XX
XX Disclosure; SEQ ID NO 15; 141pp; English.
XX
XX The invention describes an isolated polynucleotide (I) encoding a peptide
CC selected from 21 polynucleotides fully given in the specification, or the
CC complement of the polynucleotide. Also described are: an isolated peptide
CC selected from 21 peptides fully given in the specification; a host cell
CC comprising (I) or the peptide; an antibody that specifically recognizes
CC and binds the peptide; a composition comprising the host cell, the
CC peptide, or the antibody, and a pharmaceutical carrier; an immune
CC effector cell raised in the presence and at the expense of a host cell;
CC and a method for eliciting a cytolytic response in a subject. Also
CC disclosed are: a method for monitoring gene expression; a method for
CC modulating the expression of the immunomodulatory polynucleotides and
CC expression products; a method for screening for candidate agents that
CC modulate the expression of the polynucleotide or the expression products
CC of the polynucleotide; assays for the identification, assessment, and
CC development of candidate agents capable of modulating the activity of the
CC polynucleotides or polypeptides; a method for monitoring an immune
CC response in a subject; and a method for active immunotherapy. The
CC polynucleotides (e.g., blood factor domains) having immunomodulatory
CC activity are useful for detecting, diagnosing, prognosing, or monitoring
CC the progression of a disease. They are useful for aiding in the diagnosis
CC or treating disorders relating to the immune responses, e.g. cancers,
CC autoimmune diseases, or viral infections. This sequence encodes
CC immunomodulatory gene LST-1 membrane receptor alternative spliced soluble
CC form.
XX
XX SQ Sequence 6853 BP; 1798 A; 1724 C; 1832 G; 1499 T; 0 U; 0 Other;
XX
XX Alignment Scores:
Pred. No.: 3.52e-65 Length: 6853
Score: 853.50 Matches: 186
Percent Similarity: 52.7% Conservative: 0
Best Local Similarity: 52.7% Mismatches: 0
Query Match: 80.0% Indels: 167
DB: 14 Gaps: 2
US-10-696-259-6 (1-201) x ADW38506 (1-6853)
Qy 16 SerCysAlaLeuTyrValSerGlnProGluIleArgThrLeuGluGlySerSerAla 35
Db 5220 TCCTGTGCTCTCTGGGTGCCAGCCCTCGAGATTCTGATCCCTGGAGGATCTCTGCCC 5161
Qy 36 PheLeuProCysSerPheAsnAlaSerGlnGlyArgLeuAlaIleGlySerValThrTrp 55
Db 5160 TTCCTGCCCTGCTCTTCAATGCCAGCCAGGAGACTGGCCATTGGCTCCGTCACGTGG 5101
Qy 56 PheArgAspGluValValProGlyLysGluValArgAsnGlyThrProGluPheArgGly 75
Db 5100 TTCGAGATGAGTGGTTCAGGGAAGGAGGTGAGGAATGAAACCCAGAGTTTCAGGGGC 5041
Qy 76 ArgLeuAlaProLeuAlaSerSerArgPheLeuHisPheHisGlnAlaGluLeuHisIle 95
Db 5040 CGCTGGCCCCACTTGTCTTCCCGTTCTTCATGACACCCAGGCTGAGCTGCACATC 4981
Qy 96 ArgAspValArgGlyHisAspAlaSerIleTyrValCysArgValGluValLeuGlyLeu 115

Db 4980 CGGACCTGGCAGGCCATGACGCCAGCATCTACGTGTGCAGAGTGGAGTGTCTGGCCCTT 4921
Qy 116 GlyValGlyThrGlyAsnGlyThrArgLeuValValGluLys----- 129
Db 4920 GGTGTGGGACAGGGAATGGACTCGGCTGTGTGTGGAGAAAGGTGAGATGCTGGGAGGT 4861
Qy 129 ----- 129
Db 4860 GGTGTCTCTCTCTGGTGGAGGCCCAAGAGCAATGTCTTGGGAGGAGGATGTCTCC 4801
Qy 129 ----- 129
Db 4800 TCTGAGGCCCTTCTCTCTCTGAGCCTGTGTGCATCTTCTTCCCAACCCCGTCTCCATT 4741
Qy 130 -----GluHisProGlnLeuGlyAlaGlyThrValLeuLeuLeuArgAlaGlyPhe 146
Db 4740 GCCCATGCGAGAACATCTCTAGTAGGGGTGGTACAGTCTCTCTCTCTGGGTGGATT 4681
Qy 146 eTyrAlaValSerPheLeuSerValAlaValGlySerThrValTyrTyrGlnGlyLysC 166
Db 4680 CTATGCTGTGAGCTTTCTCTCTGTGGCGGTGGGCGAGCACCGTCTATTACAGGGCAATG 4621
Qy 166 s----- 166
Db 4620 TGAGTAATGGAGCCAGGGGCAATAGTGGACGGGATGGGGGCGAGTAAGAGAGTGGAG 4561
Qy 166 ----- 166
Db 4560 GAGGAGGACAGAGACCCAGGAAGAGAGAGCCCTGGGAGTGCACACTGAGCAGCTCCTG 4501
Qy 166 ----- 166
Db 4500 TCCTCTCTTGACCAGGCCACTGTACATGGGAACACACTGCCACTCTCAGATGGGCC 4441
Qy 166 ----- 166
Db 4440 CGAGGAGTGATTCCAGAGCCAGATGTCCCTAGTCTCTTCAAAGAGCCCAATAAATCT 4381
Qy 166 ----- 166
Db 4380 GCCCCACCACTAATCTCTCATGAGTCTCAAGTGTCTTCTTCTCATTTCTCAGATGCCAA 4321
Qy 167 -----LeuThrTrpL 170
Db 4320 ATCTACTCTCTCCGATTCCCCCAACTCTGAACCTTTCCCTTCCACACAGTCTGACCTGGA 4261
Qy 170 YsGlyProArgArgGlnLeuProAlaValValProAlaProLeuProProProCysGly 190
Db 4260 AAGGTCCAAGAGGAGCAGTCCGCTGTGGTCCAGGCGCCCTCCACACCAATGTGGGA 4201
Qy 190 erSerAlaHisLeuLeuProProValProGlyGly 201
Db 4200 GCTCAGCACATCTGCTTCCCTCCAGGAGGC 4166
RESULT 15
AA59347
ID AA59347 standard; cDNA; 671 BP.
XX
XX AA59347;
AC
XX
XX 20-SEP-1999 (first entry)
DT
XX
XX Human B-cell myelin oligodendrocyte glycoprotein BMOG cDNA.
DE
XX MBOG; B-cell myelin oligodendrocyte glycoprotein; human;
KW signal transduction; immunomodulator; antiinflammatory;
KW autoimmune disease; inflammation; gene therapy; diagnosis; ss.
XX Homo sapiens.
OS
XX Key Location/Qualifiers
FH CDS 66..637
FT

```
FT      /*tag= a
FT      /transl_except= (pos:291..292, aa:Arg)
FT      /note= "this codon contains an apparent 1 nucleotide
FT      deletion, which alters the reading frame"
FT      66..101
FT      sig_peptide
FT      /*tag= b
FT      102..634
FT      mat_peptide
FT      /*tag= c
FT
XX
PN      WO9923867-A2.
XX
PD      20-MAY-1999.
XX
PF      05-NOV-1998; 98WO-US023826.
XX
PR      07-NOV-1997; 97US-0064761P.
XX
PA      (BIOJ ) BIOGEN INC.
XX
PI      Browning J;
XX
XX      WPI; 1999-418423/35.
DR      P-PSDB; AAY06401.
XX
XX      Novel B-cell myelin oligodendrocyte glycoproteins.
XX
PS      Claim 1; Page 40; 43pp; English.
XX
XX      This DNA sequence encodes human BMOG, a novel member of the B cell myelin
XX      oligodendrocyte glycoprotein family that is expressed by germinal centre
XX      B cells. 3 C-terminal splice variants (see AAY06401-03) of BMOG were
XX      identified. The protein is present primarily in the spleen, in lymph
XX      nodes and in germinal centre B cells. It may have immunoregulatory
XX      functions, and soluble or chimeric fusion proteins of BMOG may be used to
XX      regulate the immune system in autoimmune or inflammatory disease. Vectors
XX      comprising BMOG, prokaryotic and eukaryotic host cells, and a method of
XX      producing BMOG using these transformed host cells are also provided. BMOG
XX      polypeptides can be used for modulating the immune system of a subject or
XX      to inhibit signal transduction in a cell expressing BMOG by contacting it
XX      with a soluble BMOG protein. The nucleic acid can be used for gene
XX      therapy. The protein can also be used to target a toxin, imaging agent or
XX      radionuclide to a cell expressing BMOG. (All claimed.)
XX
SQ      Sequence 671 BP; 124 A; 211 C; 184 G; 152 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:      6.46e-66      Length:      671
Score:      848.00      Matches:      172
Percent Similarity:      89.7%      Conservative:      2
Best Local Similarity:      88.7%      Mismatches:      8
Query Match:      79.5%      Indels:      13
DB:      2      Gaps:      2

US-10-696-259-6 (1-201) x AAX59347 (1-671)

QY      1 MetAlaTrpMetLeuLeuLeuLeuLeuMetValHisProGlySerCysAlaLeuTrp 20
Db      66 ATGGCTGGATGCTGTTGCTCATCTTGATCATGGTCCATCCAGGATCCTGTCTCTGG 125
QY      21 ValSerGlnProProGluLeuArgThrLeuGluGlySerSerAlaPheLeuProCysSer 40
Db      126 GTGTCCAGCCCCCTGAGATTCGTACCTCGAAGGATCCTCTGCTCTCTGCTCTCC 185
QY      41 PheAsnAlaSerGlnGlyArgLeuAlaLeuGlySerValThrTrpPheArgGluVal 60
Db      186 TTCAATGCCAGGCAAGGGAGACTGGCCATTGGCTCCGTCCATCCAGGATTCAGAGTGGTG 245
QY      61 ValProGlyLysGluValArgAsnGlyThrProGluPheArgGlyArgLeuAlaProLeu 80
Db      246 GTTCCAGGGAGAGGGTGGAGATGGAAACCCAGAGTTTCAG-GGGCGCTGGCCCCACTT 304
QY      81 AlaSerSerArgPheLeuHisAspHisGlnAlaGluLeuHisIleArgAspValArgGly 100
```

```
Db      305 GCTTCTTCCGTTTCTCTCCATGACCACAGGCTGAGCTGCACATCCGGGACGTGCCAGGC 364
QY      101 HisAspAlaSerIleTyrValCysArgValGluValLeuGlyLeuGlyValGlyThrGly 120
Db      365 CATGACGCCAGCATCTACGTGTGCAGAGTGGAGTGTCTGGGCTTGGTGTCCGGACAGGG 424
QY      121 AsnGlyThrArgLeuValValGluLysGluHisProGlnLeuGlyAlaGlyThrValLeu 140
Db      425 AATGGGACTCGGCTGGTGGTGGAGAAACATCCTCAGCTAGGGGCTGGTACAGTCTCTC 484
QY      141 LeuLeuArgAlaGlyPheTyrAlaValSerPheLeuSerValAlaValGlySerThrVal 160
Db      485 CTCCTTCGGGCTGGATTCTATGCTGTCTCTCTGTGGCCGTGGCGACACCGTC 544
QY      161 TyrTyrGlnGlyLys-----CysLeuThrTrpLysGlyPro 172
Db      545 TATTACAGGGCAATGCCACTGTACATGGGAACACACTGCCCACTCTCAGATGGGCC 604
QY      173 ArgArgGlnLeuProAlaValProAlaProAlaProLeuProPro 186
Db      605 CGA-----GGAGTGATTCCAGAGCCAGAGATGTCCC 634
```

Search completed: February 28, 2006, 09:14:55
Job time : 600 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: February 28, 2006, 06:33:58 ; Search time 3876 Seconds
(without alignments)
2426.265 Million cell updates/sec

Title: US-10-696-259-6
Perfect score: 1067
Sequence: 1 MAMWLLILIMVHPCALW.....APLPPCGSSAHLPPVPGG 201

Scoring table: BLOSUM62
-Q=/abs/ABSSREB spool/US10696259/runat 27022006 123556 27156/app query.fasta_1
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+ p2n.model -DEV=xlh
-Q=/abs/ABSSREB spool/US10696259/runat 27022006 123556 27156/app query.fasta_1
-DB=EST -QFMT=fastcap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPFCU=0 -LOOPEXT=0
-UNITIS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abs07
-USER=US10696259 @CGN 1.1 5315 @runat 27022006 123556 27156 -NCPU=6 -ICPU=3
-NO MMAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:*
1: gb_est1.*
2: gb_est2.*
3: gb_est3.*
4: gb_hc.*
5: gb_est4.*
6: gb_est5.*
7: gb_est6.*
8: gb_est7.*
9: gb_gss1.*
10: gb_gss2.*
11: gb_gss3.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1025	96.1	1087	4 BC018752	BC018752 Homo sapi
2	1015	95.1	1052	3 BM561738	BM561738 AGENCOURT
3	1004	94.1	878	2 BG745027	BG745027 602723117
4	988	92.6	841	3 BM561953	BM561953 AGENCOURT
5	988	92.6	1040	3 BQ053062	BQ053062 AGENCOURT
6	906	84.9	949	3 BQ053083	BQ053083 AGENCOURT
7	876	82.1	573	11 DQ052145	DQ052145 Homo sapi

8	869	81.4	573	11 DQ052146	DQ052146 Pan trogl
9	861.5	80.7	978	2 BG744192	BG744192 602722992
10	845.5	79.2	913	2 BG341330	BG341330 602463806
11	841	78.8	741	2 BG744854	BG744854 602722992
12	706.5	66.2	809	2 BG744382	BG744382 602723117
13	653	61.2	637	2 BG398004	BG398004 602439532
14	643	60.3	574	3 BM363549	BM363549 BS320057A
15	620	58.1	719	1 AM967444	AM967444 EST379519
16	593	55.6	541	3 BM364334	BM364334 BS3100020
17	578	54.2	523	3 BM364807	BM364807 BS3200050
18	557	52.2	508	3 BM364361	BM364361 BS3100020
19	534	50.0	505	6 CB428714	CB428714 604459 MA
20	516.5	48.4	451	1 AA262074	AA262074 z621a05.s
21	487	45.6	980	3 BQ053262	BQ053262 AGENCOURT
22	482	45.2	503	5 BX283861	BX283861
23	478	44.8	501	5 BX283089	BX283089
24	458	42.9	440	1 AA846055	AA846055 ak79e02.s
25	398	37.3	505	3 BM088311	BM088311 501749 MA
26	395	37.0	872	3 BQ053092	BQ053092 AGENCOURT
27	390	36.6	353	6 CB428376	CB428376 604075 MA
28	390	36.6	1639	3 BM917537	BM917537 AGENCOURT
29	378	35.4	492	1 AA237100	AA237100 z801h06.r
30	351	32.9	471	1 AA894045	AA894045
31	327	30.6	379	1 AA236886	AA236886 z801h06.s
32	289	27.1	308	2 BF522619	BF522619 UI-R-C3-s
33	287	26.9	374	7 CR464436	CR464436 CR464436
34	283.5	26.6	480	1 AV599289	AV599289 AV599289
35	268	25.1	354	1 A1511264	A1511264 UI-R-C3-s
36	256	24.0	282	1 BM308336	BM308336 3497 MARC
37	228	21.4	311	1 AW971514	AW971514 EST383603
38	185	17.3	182	1 AA721754	AA721754 nx82d04.s
39	144.5	13.5	630	1 AL878396	AL878396 AL878396
40	144.5	13.5	739	8 DR850889	DR850889 JGI_CABE1
41	144.5	13.5	803	8 DN098981	DN098981 JGI_CABE1
42	144.5	13.5	861	8 CX747707	CX747707 JGI_AHP6
43	143	13.4	1089	10 CL037400	CL037400 CHZ16-43D
44	137.5	12.9	690	5 BX773925	BX773925 BX773925
45	136.5	12.8	560	2 BE371457	BE371457 601223157

ALIGNMENTS

BC018752 1087 bp mRNA linear HTC 19-NOV-2003
Homo sapiens natural cytotoxicity triggering receptor 3, mRNA (cdna
Clone IMAGE:4849421), containing frame-shift errors.
BC018752
BC018752.1 GI:17511805
HTC.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 1087)
Srausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
Altschul,S.F., Zeeberg,B., Buettow,K.H., Schaefer,C.F., Bhat,N.K.,
Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J.J., Heiseh,F.,
Datchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
Aramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
Fahey,J., Helton,E., Kettelman,M., Madan,A., Rodrigues,S.,
Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,

Schnarch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
 Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
 12477932
 2 (bases 1 to 1087)
 Strauberg, R.
 Direct Submission
 Submitted (07-DEC-2001) National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA
 NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 Contact: MGC help desk
 Email: cgapbs-rc@mail.nih.gov
 Tissue Procurement: Dr. Daniel McVicar, DBS/NCI
 cDNA Library Preparation: Rubin Laboratory
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Genome Sequence Centre,
 BC Cancer Agency, Vancouver, BC, Canada
info@bcgsc.bc.ca
 Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,
 Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,
 Letticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo
 Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven
 Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline
 Schein, Duane Smalius, Michael Smith, Lorraine Spence, Jeff Stodd,
 Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,
 George Yang, Scott Zuyderduyn, Marco Marra.

Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRAL Plate: 40 Row: 1 Column: 12
 This clone was selected for full length sequencing because it
 passed the following selection criteria: matched mRNA gi: 24475831
 This clone has the following problem: frame shifted.

FEATURES

Location/Qualifiers
 1..1087
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:4849421"
 /tissue_type="Blood, natural killer cell"
 /clone_lib="NIH MGC_106"
 /lab_host="DH10B-R"
 /note="Vector: pOTB7"

ORIGIN

Alignment Scores:
 Pred. No.: 7,02e-86 Length: 1087
 Score: 1025.00 Matches: 200
 Percent Similarity: 90.9% Conservative: 0
 Best Local Similarity: 90.9% Mismatches: 1
 Query Match: 96.1% Indels: 19
 DB: 4 Gaps: 1
 US-10-696-259-6 (1-201) x BC018752 (1-1087)

QY 1 MetAlaTrpMetLeuLeuLeuLeuLeuLeuMetValHisProGlySerCysAlaLeuTrp 20
 DB 229 ATGGCTGGATGCTGTGCTCATCTTGATCTGATGGTCCATCCAGGATCCTGTGCTCTCGG 288
 QY 21 ValSerGlnProProGluLeuLeuArgThrLeuGluGlySerSerAlaPheLeuProCysSer 40
 DB 289 GTGTCCCAAGCCCCGAGATTCTGATCCCTGGGAAGGATCCTCTGCTTCTGTCCCTCGCTCC 348
 QY 41 PheAsnAlaSerGlnGlyArgLeuAlaIleGlySerValThrTrpPheArgAspGluVal 60
 DB 349 TTCATGTCAGCAGCAGGAGATGTCGCATTTGCTCCGTCACGTGGTTCGAGATGAGGTG 408
 QY 61 ValProGlyLyLeuValArgAsnGlyThrProGluPheArgGlyArgLeuAlaProLeu 80
 DB 409 GTTCCAGGAGAGAGGTGAGGAATGGAACCCAGAGTTTCAGGGGCGCGCTGCCCCCACTT 468

QY 81 AlaSerSerArgPheLeuHisAspHisGlnAlaGluLeuHisIleArgAspValArgGly 100
 DB 469 GCTTCTTCCCGTTCTCTCCATGACACACAGGCTGAGCTGCATCCGAGACGTGCGAGGC 528
 QY 101 HisAspAlaSerIleTrpValCysArgValGluValLeuGlyLeuGlyValGlyThrGly 120
 DB 529 CATGACGCCAGCATCTACGTGTGCAGAGTGGAGGTGCTGGGCTTGGTGTGGGACAGGG 588
 QY 121 AsnGlyThrArgLeuValValGluLysGluHisProGlnLeuGlyAlaGlyThrValLeu 140
 DB 589 AATGGACTCGGTGGTGGTGGAGAAAGAACATCTCTCAGCTAGGGGCTGGTACAGTCTCTC 648
 QY 141 LeuLeuArgAlaGlyPheTrpAlaValSerPheLeuSerValAlaValGlySerThrVal 160
 DB 649 CTCCTTCGGGCTGGATCTATGCTGTGTCAGCTTCTCTCTGTGGCCGTGGGACACCGTC 708
 QY 161 TTTTTrpGlnGlyLys-Cys----- 166
 DB 709 TATTACAGGGCAAAATATGCCAAATCTACTCTCTCGGATTCCCACTCTGAACTTTC 768
 QY 167 -----LeuThrTrpLysGlyProArgArgGlnLeuProAlaValProAl 182
 DB 769 CTTTCCACCAGGTCTGACCTGGAAAGGTCCAAAGAGGCAGCTCCGGCTGTGTCCAGC 828
 QY 182 aProLeuProProCysGlySerSerAlaHisLeuLeuProProValProGlyGly 201
 DB 829 GCCCTCTCCACCACTATGTGGAGGTTCAGCAATCTGCTTCCCCCAGTCCAGGAGGC 886
 RESULT 2
 BM561738 1052 bp mRNA linear EST 20-FEB-2002
 LOCUS
 DEFINITION
 AGENCOURT_6593503 NIH_MGC_106 Homo sapiens cDNA clone IMAGE:5484382
 S, mRNA sequence.
 ACCESSION
 VERSION
 BM561738.1 GI:18807237
 EST.
 KEYWORDS
 SOURCE
 Homo sapiens (human)
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.
 1 (bases 1 to 1052)
 NTH-MGC <http://mgc.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 CONTACT: Robert Strauberg, Ph.D.
 Email: cgapbs-rc@mail.nih.gov
 Tissue Procurement: Dr. Daniel McVicar, DBS/NCI
 cDNA Library Preparation: Rubin Laboratory
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLCM2013 row: i column: 23
 High quality sequence stop: 616.
 Location/Qualifiers
 1..1052
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5484382"
 /tissue_type="natural killer cells, cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH MGC_106"
 /note="Organ: blood; Vector: pOTB7; Site: 1: XhoI; Site 2:
 EcoRI; cDNA made by oligo-dT priming. Directionally cloned
 into EcoRI/XhoI sites using the following 5' adaptor:
 GGACAGAG(G). Library constructed by Ling Hong in the
 laboratory of Gerald M. Rubin (University of California,
 Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
 Superscript II RT (Life Technologies). Note: this is a

FEATURES

source


```

QY 160 lTyrTrpGlnGlyys-Cys----- 166
Db 296 CTATTACAGGCAATATGCCAAATCTACTCTCCGGATTCCCCCACTCTGAACCTT 237
QY 167 -----LeuThrTrpGlyProArgArgGlnLeuProAlaValValProA 182
Db 236 CCCTTCCACCAGGCTCTGACCTGGAAAGGTCCAGAGGAGTGCGGCTGTGGTCCAG 177
QY 182 laProLeuProProCysGlySerSerAlaHisLeuLeuLeuProValProGlyGly 201
Db 176 CGCCCTCCACCACCATGTGGGAGCTCAGACATCTGTTCCCCAGTCCAGGAGGC 118

RESULT 4
BM561953 841 bp mRNA linear EST 20-FEB-2002
LOCUS AGENCOURT_6593188 NIH_MGC_106 Homo sapiens cDNA clone IMAGE:5484506
DEFINITION 5', mRNA sequence.
ACCESSION BM561953
VERSION BM561953.1 GI:18807631
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE NIH-MGC http://mgs.nci.nih.gov/.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Tissue Procurement: Dr. Daniel McVicar, DBS/NCI
cDNA Library Preparation: Rubin Laboratory
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L10M2013 row: o column: 03
High quality sequence stop: 641.
FEATURES
    Location/Qualifiers
        1..841
            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /clone="IMAGE:5484506"
            /tissue_type="natural killer cells, cell line"
            /lab_host="DH10B (phage-resistant)"
            /clone_lib="NIH_MGC_106"
            /note="Organ: blood; Vector: pOTB7; Site 1: XhoI; Site 2:
            EcoRI; cDNA made by oligo-dT priming. Directionally cloned
            into EcoRI/XhoI sites using the following 5' adaptor:
            GGACGAG(G). Library constructed by Ling Hong in the
            laboratory of Gerald M. Rubin (University of California,
            Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
            Superscript II RT (Life Technologies). Note: this is a
            NIH_MGC Library."
ORIGIN
Alignment Scores:
Pred. No.: 1,54e-82 Length: 841
Score: 988.00 Matches: 193
Percent Similarity: 90.6% Conservative: 0
Best Local Similarity: 90.6% Mismatches: 1
Query Match: 92.6% Indels: 19
DB: 3 Gaps: 1

US-10-696-259-6 (1-201) x BM561953 (1-841)

QY 8 lIleuLeuMetValHisProGlySerCysAlaLeuTrpValSerGlnProGluIle 27
Db 3 ATCTTGATCATGTCATCCAGGATCCTGTGCTCTCTGCGTGTCCAGCCCCCTGAGATT 62

```

```

QY 28 ArgThrLeuGluGlySerSerAlaPheLeuProCysSerPheAsnAlaSerGlnGlyArg 47
Db 63 CGTACCTCGAAGATCCCTCTGCTTCTGCTTCTTCAATGCCACCAAGGAGA 122
QY 48 LeuAlaIleGlySerValThrTrpPheArgAspGluValValProGlyLysGluValArg 67
Db 123 CTGGCCATTGGCTCCGTCACGTGGTTCCGAGATGAGGTGGTTCCAGGGAAGGAGGTGAGG 182
QY 68 AsnGlyThrProGluPheArgGlyArgLeuAlaProLeuAlaSerSerArgPheLeuHis 87
Db 183 AATGGAAACCCAGAGTTACGGGGCCGCTGGCCCCCATCTTCTTCTCCCGTTTCTCCAT 242
QY 88 AspHisGlnAlaGluLeuHisIleArgAspValArgGlyHisAspAlaSerIleTyrVal 107
Db 243 GACCACCAAGCTGAGCTGCACATCCGGGACGTGGAGGCCATGACGCCAGCATCTACGTG 302
QY 108 CysArgValGluValLeuGlyLeuGlyValGlyThrGlyAsnGlyThrArgLeuValVal 127
Db 303 TGCAGAGTGGAGGTGCTGGGCTTGGTGTCCGGACAGGGAATGGGACTCGGCTGGTGGTG 362
QY 128 GluLysGluHisProGlnLeuGlyAlaGlyThrValLeuLeuLeuArgAlaGlyPheTyr 147
Db 363 GAGAAAGAAATCTCTCAGCTAGGGGCTGGTACAGTCTCTCTCTCGGGCTGGATTCTAT 422
QY 148 AlaValSerPheLeuSerValAlaValGlySerThrValTyrTyrGlnGlyLys-Cys-- 166
Db 423 GCTGTGAGCTTCTCTCTGTGGCGGTGGCGAGCACCGCTATTACCAGGGGCAATATATGCC 482
QY 167 -----LeuThrTyr 169
Db 483 AAATCTACTCTCTCCGGATTCCCCCACTCTGAACTTTCCCTTCCACCAAGTCTCGACCTG 542
QY 169 pLysGlyProArgArgGlnLeuProAlaValValProAlaProLeuProProCysGln 189
Db 543 GAAAGGTCACAGAGGAGGAGCTCGCGCTGTGTCCAGCGCCCTCCACCCACCATGTGG 602
QY 189 YserSerAlaHisLeuLeuProProValProGlyGly 201
Db 603 GAGCTCAGCACATCTGCTTCCCGGAGTCCCGAGGAGGC 639

RESULT 5
BM561953 1040 bp mRNA linear EST 29-MAR-2002
LOCUS AGENCOURT_6821798 NIH_MGC_106 Homo sapiens cDNA clone IMAGE:5934616
DEFINITION 5', mRNA sequence.
ACCESSION BM561953
VERSION BM561953.1 GI:19812402
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
JOURNAL Hominidae; Homo.
COMMENT NIH-MGC http://mgs.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgaabs-remail.nih.gov
Tissue Procurement: Dr. Daniel McVicar, DBS/NCI
cDNA Library Preparation: Rubin Laboratory
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Clone distribution: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L10M2121 row: a column: 17
High quality sequence stop: 748.
FEATURES
    Location/Qualifiers
        1..1040
            /organism="Homo sapiens"
            /mol_type="mRNA"

```

```

/db xref="taxon:9606"
/clone="IMAGS:5934616"
/tissue_type="natural killer cells, cell line"
/lab host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_106"
/note="Organ: blood; Vector: pOMB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCACGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH MGC Library."

```

ORIGIN

Alignment Scores:		
Pred. No.:	2.01e-82	Length:
Score:	988.00	Matches:
Percent Similarity:	90.6%	Conservative:
Best Local Similarity:	90.6%	Mismatches:
Query Match:	92.6%	Indels:
DB:	3	Gaps:
		1040
		193
		0
		1
		19
		1

US-10-696-259-6 (1-201) x BQ053062 (1-1040)

Qy	8	IleLeuIleMetValHisProGlySerCysAlaLeuTrpValSerGlnProGluIle	27
Db	2	ATCTTGATCATGGTCCATCCAGGATCCCTGTCTCTGGTGTCAGCCCCCTGAGATT	61
Qy	28	ArgThrLeuGluGlySerSerAlaPheLeuProCysSerPheAsnAlaSerGlnGlyArg	47
Db	62	CGTRACCTGGAAAGATCTCTGCCTTCTGCCTCTCTCTCAATGCCAGCCAAAGGAGA	121
Qy	48	LeuAlaIleGlySerValThrTrpPheArgAspGluValValProGlyLysGluValArg	67
Db	122	CTGGCCATTGGCTCCGTCACGTGGTTCAGATGAGTGGTTCCAGGGAAGAGGTGAGG	181
Qy	68	AsnGlyThrProGluPheArgGlyValGluLeuAlaProLeuAlaSerSerArgPheLeuHis	87
Db	182	AATGGAACCCAGAGTTTCAGGGGCGCTGGCCCCACTTGGCTTCTTCCCGTTTCTCCCAT	241
Qy	88	AspHisGlnAlaGluLeuHisIleArgAspValArgGlyHisAspAlaSerIleTrVal	107
Db	242	GACCACAGGCTGAGCTGCACATCCGGAGCGTGCAGAGCCATGACCCAGCATCTACGTG	301
Qy	108	CysArgValGluValLeuGlyLeuGlyValGlyThrGlyAsnGlyThrArgLeuValVal	127
Db	302	TGCAGAGTGGAGGTCTGGGCTTGGTGTGCGGACAGGGAAATGGGACTCGGCTGGTGGT	361
Qy	128	GluLysGluHisProGlnLeuGlyAlaGlyThrValLeuLeuLeuArgAlaGlyPheTrp	147
Db	362	GAGAAAGAAATCTTCAGCTAGGGCTGGTACAGTCTCTCTCTGGGCTGGATTCTAT	421
Qy	148	AlaValSerPheLeuSerValAlaValGlySerThrValTyrTyrGlnGlyLys-Cys--	166
Db	422	GCTGTGAGCTTCTCTCTGTGGCGTGGGACGACCGTCTATTACAGGGCAAAATATGCC	481
Qy	167	-----LeuThrTr	169
Db	482	AAATCTACTCTCCGGATTCCCCAACTCTGAACTTTTCCCTTCCACCAGGTCTGCACCTG	541
Qy	169	pLysGlyProArgArgGlnLeuProAlaValValProAlaProLeuProProProCysGln	189
Db	542	GAAGGTCCAGAGAGGAGCTGCCGGCTGTGGTCCAGGGCCCCCTCCACACCAACATGGG	601
Qy	189	ySerSerAlaHisLeuLeuProProValProGlyGly	201
Db	602	GAGCTCAGCACATCTGCTTCTCCCGAGTCCAGGAGCC	638

[illegible]

ACCESSION VERSION KEYWORDS SOURCE ORGANISM	REFERENCE AUTHORS TITLE JOURNAL COMMENT
--	---

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100

FEATURES source

ORIGIN

Alignment Scores:

Alignment Scores:			
Pred. No.:	9.35e-75	Length:	949
Score:	906.00	Matches:	184
Percent Similarity:	92.5%	Conservative:	2
Best Local Similarity:	91.5%	Mismatches:	13
Query Match:	84.9%	Indels:	3
DB:	3	Gaps:	0

US-10-696-259-6 (1-201) x BQ053083 (1-949)

Qy	1	MetAlaTrpMetLeuLeuLeuLeuLeuLeuMetValHisProGlySerCysAlaLeuTrp	20
Db	208	ATFGGCTCGATGCTGTTCCTCATCTTCATCATGCTCCAGATCCAGATCTGCTCTGG	267
Qy	21	ValSerGlnProProGluLeuArgThrLeuGluGlySerSerAlaPheLeuProCysSer	40
Db	268	GGTGTCCACAGCCCTGACATTCGTACCTGGAAAGATCCCTGTGCTTCTCGCCCTGCTCC	327

Qy	41	PheAsnAlaSerGlnGlyValTyrLeuAlaIleGlySerValThrTrpPheArgAspGluVal	60
Db	328	TTCAATGCCAGCCAGGCGAGACTGSCCATTTGGCTCCGTCACGTGGTTCGAGATGAGGTG	387
Qy	61	ValProGlyLysGluValIArgAsnGlyThrProGluPheArgGlyArgLeuAlaProLeu	80
Db	388	GTTTCAGCGAAGAGAGTGCAGAAATGGAACCCACAGATTCAGGGGCGGCTTGCCTCCACTT	447

Qy 81 AlaSerArgPheLeuHisAspHisGlnAlaGluLeuHisIleArgAspValArgGly 100
|||
Db 448 GCTTCTTCCCGTTTCTCTCATGACCAACCAAGGCTGAGCTGCACATCCGGGACGTGCAGGC 507

```
QY 101 HieAspAlaSerIleTyrValCysArgValGluValLeuGlyLeuGlyValGlyThrGly 120
Db 508 CATGACGCCAGCATCTACGTGTGCAGAGTGGAGGTGCTGGCCCTTGGTGCAGGACAGGG 567
QY 121 AsnGlyThrArgLeuValValGluLysGluHisProGlnLeuGlyAlaGlyThrVal-Le 140
Db 568 AATGGGACTCGGTGGTGGTGGAGAAAGAACATCCTCAGCTTANGGGCTGGTACAGTCCCT 627
QY 140 uLeuLeuArgAlaGlyPheTyrAlaValSerPheLeuSerValAlaValGlySerThrVa 160
Db 628 CCYCCCTTCGGGCTGGATTCTATGCTGTGCAGCTTTCTCTGTGGCCGTGGGACACCGT 687
QY 160 lTyrTyrGlnGlyLysCysLeuThrTrpLysGlyProArgGlnLeuProAlaValVa 180
Db 688 CTATTACAG-GGCNAATGTCTGACCTGAAAGGTCAAAGGCGAGCTGCCCGGTGGTT 746
QY 180 lProAlaProLeuProProProCys-GlySerSerAlaHisLeuLeuProProValPro 199
Db 747 CCCAAGGGCCCTCCACCAACATGTTGGGAGCTCACACAATCTGTTCCGCCAGTCCC 805

RESULT 7
DQ052145 573 bp DNA linear GSS 02-JUN-2005
LOCUS DQ052145
DEFINITION Homo sapiens NCR3 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
ACCESSION DQ052145
VERSION DQ052145.1 GI:66905601
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 573)
AUTHORS Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,
Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D.,
White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE A Scan for Positively Selected Genes in the Genomes of Humans and
Chimpanzees
JOURNAL (ex) PLoS Biol. 3 (6), E170 (2005)
PUBMED 15869325
REFERENCE 2 (bases 1 to 573)
AUTHORS Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,
Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D.,
White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment. Translation starts at the beginning of
alignment.
FEATURES
source Location/Qualifiers
1..573
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="6"
<1..>573
/gene="NCR3"
/locus_tag="HC20172"

gene
ORIGIN
Alignment Scores: 3.28e-72 Length: 573
Pred. No.: 876.00 Matches: 173
Score: 90.2% Conservative: 2
Percent Similarity: 89.2% Mismatches: 7
Best Local Similarity: 82.1% Indels: 12
Query Match: 11 Gaps: 2
DB:

US-10-696-259-6 (1-201) x DQ052145 (1-573)
QY 1 MetaLtrpMetLeuLeuLeuIleLeuMetValHisProGlySerCysAlaLeuTrp 20
```

```
Db 1 ATGGCCTGAGTGTGTGCTCATCTTTGATCATGTCATCCAGGATCCTGTGCTCTCTGG 60
QY 21 ValSerGlnProGlnIleArgThrLeuGluGlySerSerAlaPheLeuProCysSer 40
Db 61 GTGTCCAGGCCCTCAGATTGTCCTCCCTGGAAGGATCCTCTGCCCTTCCTGCCCTGCTCC 120
QY 41 PheAsnAlaSerGlnGlyArgLeuAlaIleGlySerValThrTrpPheArgAspGluVal 60
Db 121 TTCAATGCCAGCCAGGAGACTGGCCATTGGCTCCGTACAGTGGTTCCGAGATGAGGTG 180
QY 61 ValProGlyLysGluValArgAsnGlyThrProGlnPheArgGlyArgLeuAlaProLeu 80
Db 181 GTTCCAGGGAAGGAGGTGAGGAATGGAACCCAGAGTTTCAGGGGCCCTTGGCCCCACTT 240
QY 81 AlaSerSerArgPheLeuHisAspHisGlnAlaGluLeuHisIleArgAspValAlaGly 100
Db 241 GCTTCTTCCTCCGTTTCCTCCATGCCACAGGCTGAGCTGCACATCCGGGACGTGCGAGGC 300
QY 101 HisAspAlaSerIleTyrValCysArgValGluValLeuGlyLeuGlyValGlyThrGly 120
Db 301 CATGACGCCAGCATCTACGTGTGCAGAGTGGAGGTGCTGGCCCTTGGTGCAGGACAGG 360
QY 121 AsnGlyThrArgLeuValValGluLysGluHisProGlnLeuGlyAlaGlyThrValLeu 140
Db 361 AATGGGACTCGGTGGTGGTGGAGAAAGAACATCCTCAGCTAGGGGCTGGTACAGTCTCTC 420
QY 141 LeuLeuArgAlaGlyPheTyrAlaValSerPheLeuSerValAlaValGlySerThrVal 160
Db 421 CTCCTTCGGGCTGGATTCTATGCTGTGCAGCTTTCTCTGTGGCCGTGGGACGACCGTC 480
QY 161 TyrTyrGlnGlyLys-----CysLeuThrTrpLysGlyPro 172
Db 481 TATTACCGGGCAATGCCACTGTGCATGGGAACACACTGCCACTCCTCAGATGGGCC 540
QY 173 ArgArgGlnLeuProAlaValValProAlaProLeuProPro 186
Db 541 CGA-----GGAGTGATTCCAGAGCCAGATGTCCC 570

RESULT 8
DQ052146 573 bp DNA linear GSS 02-JUN-2005
LOCUS DQ052146
DEFINITION Pan troglodytes NCR3 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
ACCESSION DQ052146
VERSION DQ052146.1 GI:66905602
KEYWORDS GSS.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Pan.
REFERENCE 1 (bases 1 to 573)
AUTHORS Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,
Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D.,
White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE A Scan for Positively Selected Genes in the Genomes of Humans and
Chimpanzees
JOURNAL (ex) PLoS Biol. 3 (6), E170 (2005)
PUBMED 15869325
REFERENCE 2 (bases 1 to 573)
AUTHORS Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,
Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D.,
White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment. Translation starts at the beginning of
alignment.
FEATURES
source Location/Qualifiers
1..573
/organism="Pan troglodytes"
```

JOURNAL
COMMENT

/mol_type="genomic DNA"
/db_xref="taxon:9598"
<1..>573
/gene="NCR3"
/locus_tag="HC20172"

gene

ORIGIN

Alignment Scores:

Pred. No.: 15e-71 Length: 573
Score: 869.00 Matches: 172
Percent Similarity: 89.7% Conservative: 2
Best Local Similarity: 88.7% Mismatches: 8
Query Match: 81.4% Indels: 12
DB: 11 Gaps: 2

US-10-696-259-6 (1-201) x DQ052146 (1-573)

Qy 1 MetAlaTrpMetLeuLeuLeuLeuLeuLeuMetValHisProGlySerCysAlaLeuTrp 20
Db 1 ATGGCCTGGAGTCTGTGCTCATCTTGATCATGTGTCATCCAGGATCCTGTGCTCTCGG 60
Qy 21 ValSerGlnProProGluLeuArgThrLeuGluGlySerSerAlaPheLeuProCysSer 40
Db 61 GTGTCCAGCCCTCGAGATTCGTACCTCGAAGGATCCTCTGCTTCTGCTCTGCTCTCC 120
Qy 41 PheAsnAlaSerGlnGlyArgLeuAlaIleGlySerValThrTrpPheArgAspGluVal 60
Db 121 TTCAATGCCAGCAAGGAGACTGGCCATTGGCTCCGTCACGTGGTTCGAGATGAGGTG 180
Qy 61 ValProGlyLysGluValArgAsnGlyThrProGluPheArgGlyArgLeuAlaProLeu 80
Db 181 GTTCCAGGGAAGGAGGTGAGAAATGAACCCCGAGTTTCAGGGCGCGCTGGCCCACTT 240
Qy 81 AlaSerArgPheLeuHisAspHisGlnAlaGluLeuHisIleArgAspValArgGly 100
Db 241 GCTTCTTCCGTTTCTTCATGACACACAGGCTGAGCTGACATCCGGGAGCTGCGAGGC 300
Qy 101 HisAspAlaSerIleTyrrValCysArgValGluValLeuGlyLeuGlyValGlyThrGly 120
Db 301 CATGACGCCAGCATCTACGTGTGCAGAGTGGAGGTGTGTGGGCTTGTGTGCGGACAGG 360
Qy 121 AsnGlyThrArgLeuValValGluLysGluHisProGlnLeuGlyAlaGlyThrValLeu 140
Db 361 AATGGGACTCGGCTGGTGGTGGAGAAAGAACATCTCAGCTAGGGGCTGTGTACAGTCTC 420
Qy 141 LeuLeuArgAlaGlyPheTyrrAlaValSerPheLeuSerValAlaValGlySerThrVal 160
Db 421 CTCCTTCGGGCTGGATTCTATGCTGTCTGCTGTCTCTGTGGCGCGTGGCGAGCACCGTC 480
Qy 161 TyrTyrrGlnGlyLys-----CysLeuThrTrpLysGlyPro 172
Db 481 TATTACCAGGGCAAAATGCCACTGTACATGGGAACACACTGCCACTCCTCAGATGGGCC 540
Qy 173 ArgArgGlnLeuProAlaValValProAlaProLeuProPro 186
Db 541 CGA-----GGAGTGTATTCAGAGGCCAGAGGTCCC 570

RESULT 9
BG744192 978 bp mRNA linear EST 15-MAY-2001
LOCUS 60272292F1 NIH_MGC_106 Homo sapiens cDNA clone IMAGE:4849222 5',
DEFINITION mRNA sequence.

ACCESSION BG744192
VERSION BG744192.1 GI:14054845
KEYWORDS EST.

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo

REFERENCE 1 (bases 1 to 978)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Daniel McVicar, DBS/NCI
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>

Plate: LICM1688 row: h column: 23

High quality sequence stop: 802.

FEATURES
source

1..978
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4849222"
/tissue_type="natural killer cells, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 106"
/note="Organ: blood; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."

ORIGIN

Alignment Scores:

Pred. No.: 15e-70 Length: 978
Score: 861.50 Matches: 172
Percent Similarity: 86.3% Conservative: 4
Best Local Similarity: 84.3% Mismatches: 21
Query Match: 80.7% Indels: 7
DB: 2 Gaps: 3

US-10-696-259-6 (1-201) x BG744192 (1-978)

Qy 1 MetAlaTrpMetLeuLeuLeuLeuLeuMetValHisProGlySerCysAlaLeuTrp 20
Db 265 ATGGCCTGGATGTGTGCTCATCTTGATCATGTGTCATCCAGGATCCTGTGCTCTCGG 324
Qy 21 ValSerGlnProProGluLeuArgThrLeuGluGlySerSerAlaPheLeuProCysSer 40
Db 325 GTGTCCAGGCCCTCGAGATTGCTGACCTGGAAGGATCCTCTGCTCTTCTGCTCTGCTCC 384
Qy 41 PheAsnAlaSerGlnGlyArgLeuAlaIleGlySerValThrTrpPheArgAspGluVal 60
Db 385 TTCAATGCCAGCCAGCAGGAGACTGGCCATTGGCTCCGTACAGTGTTCGAGATGAGGTG 444
Qy 61 ValProGlyLysGluValArgAsnGlyThrProGluPheArgGlyArgLeuAlaProLeu 80
Db 445 GTTCCAGGGAAGGAGGTGAGAAATGGGACCCAGAGTTTCAGGGCGCGCTGGCCCACTT 504
Qy 81 AlaSerSerArgPheLeuHisAspHisGlnAlaGluLeuHisIleArgAspValArgGly 100
Db 505 GCTTCTTCCGCTTCTTCATGACACACAGGCTGAGCTGCACATCCGGGAGCTGCGAGGC 564
Qy 101 HisAspAlaSerIleTyrrValCysArgValGluValLeuGlyLeuGlyValGlyThrGly 120
Db 565 CATGACGCCAGCATCTACGTGTGCAGAGTGGAGGTGTGTGGGCTTGTGTGCGGACAGG 624
Qy 121 AsnGlyThrArgLeuValValGluLysGluHisProGlnLeuGlyAlaGlyThrValLeu 140
Db 625 AATGGGACTCGGCTGGTGGTGGAGAAAGAACATCTCAGCTAGGGGCTGTGTACAGTCTC 684
Qy 141 LeuLeuArgAlaGlyPheTyrrAlaValSerPheLeuSerValAlaValGlySerThrVal 160
Db 685 CTCCTTCGGGCTGGATTCTATGCTGTCTGCTCTCTCTGTGAGCGTGGGCGAGCACCGTC 744

```

QY 161 TTTTCTGlnGlyLysCysLeuThrTrpLys-----GlyProArgArgGlnLeuProAla 178
Db 745 TATTACAGGCAATATGCCAAATCTACTCTCTGGATTCCTCCCAATCTGAACCTCCCTCC 804
QY 179 ValVal---ProAlaProLeuProProProCys-----GlySerSerAlaHis 193
Db 805 ACGGTCTGACTGGAAGTCCAGACGAGGTGGCGGTGGCGCCAGGCGCTCCCAACAC 864
QY 194 LeuLeuProPro 197
Db 865 ATGTGGGAGCCA 876

RESULT 10
BG341330 913 bp mRNA linear EST 27-FEB-2001
LOCUS 602463806f1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4576657 5',
DEFINITION mRNA sequence.
ACCESSION BG341330
VERSION BG341330.1 GI:13147768
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
1 (bases 1 to 913)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov row: 1 column: 02
Plate: L1CMI289 row: 1 column: 02
High quality sequence stop: 781.
FEATURES
Location/Qualifiers
1..913
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4576657"
/tissue_type="primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 48"
/notes="Organ: B-cells; Vector: pOTB7; Site:1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

ORIGIN
Alignment Scores:
Pred. No.: 4,4e-69 Length: 913
Score: 845.50 Matches: 180
Percent Similarity: 82.4% Conservative: 2
Best Local Similarity: 81.4% Mismatches: 11
Query Match: 79.2% Indels: 30
DB: 2 Gaps: 2

US-10-696-259-6 (1-201) x BG341330 (1-913)

QY 9 LeuLeuMetValHisProGly-----SerCysAlaLeu 19
Db 60 TTGATGCTCGAGTCCCTGGCAGTTGTGTCTTGGCAAGTGTATGTGATCCTGTGCTCTC 119

```

```

QY 20 TrpValSerGlnProGluIleArgThrLeuGluGlySerSerAlaPheLeuProCys 39
Db 120 TGGGTGTCCAGCCCCCTGAGATTCGACCTCGAAGGATCCTCTGCCTTCCTGCCCTGC 179
QY 40 SerPheAsnAlaSerGlnGlyArgLeuAlaIleGlySerValThrTrpPheArgAspGlu 59
Db 180 TCCTTCAATGCCAGCAAGGAGGAGCTGGCCATTGGCTCCGTCACGTGGTTCGAGATGAG 239
QY 60 ValValProGlyLysGluValArgAsnGlyThrProGluPheArgGlyArgLeuAlaPro 79
Db 240 GTGGTTCCAGGAAG-GAGGTGAGGAATGGAAACCCAGAGTTCAGGTGCCCTCCGCCCA 298
QY 80 LeuAlaSerSerArgPheLeuHisAspHisGlnAlaGluLeuHisIleArgAspValArg 99
Db 299 CTTGCTTCTTCCCGTTTCTCCATGACCACACAGGCTGAGCTGCACATCCGGGAGTGCGA 358
QY 100 GlyHisAspAlaSerIleThrValCysArgValGluValLeuGlyLeuGlyValGlyThr 119
Db 359 GGCCATGACGCCAGCATCTACGTGTGCAGAGTGAGGTGCTGGGCTTGGTGTGCGGACA 418
QY 120 GlyAsnGlyThrArgLeuValValGluLysGluHisProGlnLeuGlyAlaGlyThrVal 139
Db 419 GGGAAATGGGACTCGGCTGGTGGTGGAGAAACATCCTCAGCTAGGGGCTGGTACAGTC 478
QY 140 LeuLeuLeuArgAlaGlyPheTyrAlaValSerPheLeuSerValAlaValGlySerThr 159
Db 479 CTCCTCCTTCGGGCTGGATCTATGCTCAGCTTCTCTCTGTGGGCGTGGGAGCACC 538
QY 160 ValTyrTyrGlnGlyLys----- 165
Db 539 GTCTATTACCAGGCAAAATATGCCAAATCTACTCTCCGATCCGCCAATCTCAACTTT 598
QY 166 -----CysLeuThrTrpLysGly-ProArgArgGlnLeuProAlaValPr 181
Db 599 CCCTTCCACCAGGTCTGGACCTGGACAGGTCCCAAGGAGCAGCTGCGGCTGGTCCC 658
QY 181 oAlaProLeuProProCysGlySerSerAlaHisLeuLeuProProValProGlyVGL 201
Db 659 AGCCGCCCTCCACCACACA-AGTGGGAGCTAGCACATCTGCTTCCCCCAGTCCAGGAGG 717
QY 201 Y 201
Db 718 T 718

RESULT 11
BG744854/c 741 bp mRNA linear EST 15-MAY-2001
LOCUS 602722992T1 NIH_MGC_106 Homo sapiens cDNA clone IMAGE:4849222 3',
DEFINITION mRNA sequence.
ACCESSION BG744854
VERSION BG744854.1 GI:14055507
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
1 (bases 1 to 741)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Daniel McVicar, DBS/NCI
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov row: h column: 23
Plate: L1CMI688 row: h column: 23
High quality sequence stop: 741.

```



```

Qy 101 HisAspAlaSerIleTyr---ValCysArgValGluValLeuGlyLeuGlyValGlyThr 119
Dy 530 CATGACGCCAGCATCTACCGTGTGCACGAGTGGCAGGTGCTGGGCTTGGTGTGGGACC 589
Qy 120 -GlyAsnGlyThrArgLeuValValGlu-LysGluHisProGlnLeuGlyAlaGly-Thr 138
Dy 590 AGGAATGGGACTCGGCTGGTGTGCACGACCGCAACCTCCTCAGCTACGCGCTGGCTACA 649
Qy 139 ValLeuLeuLeuArg-AlaGlyPheTyrAlaValSerPheLeu-SerValAlaValGlyS 158
Dy 650 GTCTCTCTCTTCGGGCTGCATTCTATGTGTGTGAGCTTTCTTCTGTGGCCGTGGGCA 709
Qy 158 erThrValTyrGlnGlyLys 165
Dy 710 GCACCGTCTATCACCAGGCCCA 732

RESULT 13
BG398004 602439532F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4565983 5',
LOCUS mRNA sequence.
DEFINITION BG398004.1 GI:13291452
ACCESSION BG398004
VERSION BG398004.1
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 637)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCMI283 row: o column: 08
High quality sequence stop: 628.
FEATURES
Location/Qualifiers
source 1..637
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4565983"
/tissue_type="primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_48"
/note="Organ: B-cells; Vector: pOTB7; Site 1: XhoI;
Site 2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GCCACAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

ORIGIN
Alignment Scores:
Pred. No.: 3.64e-51 Length: 637
Score: 653.00 Matches: 131
Percent Similarity: 97.1% Conservative: 1
Best Local Similarity: 96.3% Mismatches: 3
Query Match: 61.2% Indels: 2
DB: 2 Gaps: 0

US-10-696-259-6 (1-201) x BG398004 (1-637)

```

```

Qy 1 MetAlaTrpMetLeuLeuLeuLeuLeuLeuMetValHisProGlySerCysAlaLeuTrp 20
Dy 230 ATGCCCTGGGATGCTTGTGGCTCACTTGTATCATGTCATCCAGATCCTGTGCTCTCTGG 289
Qy 21 ValSerGlnProProGluIleArgThrLeuGluGlySerSerAlaPheLeuProCysSer 40
Dy 290 GTGTCCAGCCCCCTGAGATTGTAACCTGGAAGGATCCTCTGCCTTCCTGCCCTGTCTCC 349
Qy 41 PheAsnAlaSerGlnGlyArgLeuAlaIleGlySerValThrTrpPheArgAspGluVal 60
Dy 350 TTCAATGCCAGCAAGGAGACATGGCCATTGGTCTCCGTCACGTGTTCCGAGATGAGGTG 409
Qy 61 ValProGlyLysGluValArgAsnGlyThrProGluPheArgGlyArgLeuAlaProLeu 80
Dy 410 GTTCCAGGAAG-GAGGTGAGGAATGGAACCCAGAGTTCAGGCGCCCTGGCCCCACTG 468
Qy 81 -AlaSerSerArgPheLeuHisAspHisGlnAlaGluLeuHisIleArgAspValArgG1 100
Dy 469 TGCTTCTTCCCGTTTCTTCATGACCACAGGCTGAGTCACATCCGGGACGTGCGAGG 528
Qy 100 yHisAspAlaSerIleTyrValCysArgValGluValLeuGlyLeuGlyValGlyThrG1 120
Dy 529 CCATGACGCCAGCATCTACGTGTGCAGAGTGGAGGTGCTGGGCTTGTGTCGGGACAGG 588
Qy 120 yAsnGlyThrArgLeuValValGluLysGluHisProGlnLeuGly 135
Dy 589 GAATGGGACTCGGCTGGTGTGGAGAAAGACCATCTCAGTAGGGG 634

RESULT 14
BM363549 574 bp mRNA linear EST 10-JAN-2002
LOCUS BS320057A20D02 Subtracted Lewin Cattle Spleen cDNA clone
DEFINITION BS320057A20D02 5', mRNA sequence.
ACCESSION BM363549
VERSION BM363549
KEYWORDS EST.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bovinae; Bos.
REFERENCE 1 (bases 1 to 574)
AUTHORS Lewin, H.A., Soares, M.B., Pardinias, J., Liu, L. and Larson, J.H.
TITLE Subtracted Lewin Cattle Spleen ESTs
JOURNAL Unpublished (2002)
COMMENT Contact: Lewin, H. A.
W. M. Keck Center for Comparative and Functional Genomics
University of Illinois at Urbana-Champaign
340 Edward R. Madigan Laboratory, 1201 W. Gregory Dr., Urbana, IL
61801, USA
Tel: 217 333 5998
Fax: 217 244 5617
Email: h-lewin@uiuc.edu
Funding for Cattle EST sequencing was provided by the USDA National
Research Initiative, Project No. 98-35205-6644, and a grant from
the Japanese Ministry of Agriculture Fisheries and Forestry to
H.A.Lewin and J.E.Womack. Base-calling/Quality scores: PHRED form
Washington University Genome Center. Vector-trimming: Cross Match
from Washington University Genome Center PHRAP suite. This sequence
is vector free and at least 200bp in length.
Insert Length: 574 Std Error: 0.00
Plate: BS320057A20 row: D column: 02
Seq primer: CGCCAGCTCGAATTAACCC
High quality sequence stop: 574.
FEATURES
Location/Qualifiers
source 1..574
/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/clone="BS320057A20D02"
/sex="female"

```


/dev_stage="Adult"
/clone_libs="Subtracted Lewin Cattle Spleen"
/note="Organ: Spleen; Vector: pBluescript SK(+/-); Site 1:
EcoRI; Site 2: XhoI; This BS cDNA library was generated by
subtraction of the original non-normalized bovine spleen
library with 16,800 previously sequenced clones from a
bovine placenta cDNA library. The original library was
constructed as described by Band et al (2000), Genome
Research 10(9): 1359-1368."

ORIGIN

Alignment Scores:
Pred. No.: 2,79e-50 Length: 574
Score: 643.00 Matches: 126
Percent Similarity: 85.0% Conservative: 10
Best Local Similarity: 78.8% Mismatches: 24
Query Match: 60.3% Indels: 0
DB: 3 Gaps: 0

US-10-696-259-6 (1-201) x BM363549 (1-574)

Qy 1 MetAlaTrpMetLeuLeuLeuLeuLeuMetValHisProGlySerCysAlaLeuTrp 20
Db 93 ATGGCCAGATGCTGTGTTTCATCTTTATCATCTCGTCCAGGATCTTGTGTTCTCGG 152
Qy 21 ValSerGlnProGluLeuLeuLeuLeuGluGlySerSerAlaPheLeuProCysSer 40
Db 153 GTGTCCAGCCCTCGAATCCGTACCAGGAGGGTCCCCCGCTTCTCGCTGTTC 212
Qy 41 PheAsnAlaSerGlnGlyArgLeuAlaIleGlySerValThrTrpPheArgAspGluVal 60
Db 213 TTCAATGCCACCAAGGAGTTTGCCCAITGGTCTGTGTCATCGTACCGGGACAAGTG 272
Qy 61 ValProGlyLysGluValArgAsnGlyThrProGluPheArgGlyArgLeuAlaProLeu 80
Db 273 GCCCCAGGATGGAGGTGAGGAATCAGACCCGACAGTTCCAGGCCCGCTGCCCCCTC 332
Qy 81 AlaSerSerArgPheLeuHisAspHisGlnAlaGluLeuHisIleArgAspValArgGly 100
Db 333 CCCTCTTCCCGCTTCTCTGTGACCCAGGCTGAGTGCACATCTGGGACACCCGAGGC 392
Qy 101 HisAspAlaSerIleTyrValCysArgValGluValLeuGlyLeuGlyValGlyThrGly 120
Db 393 CGTGACACTGGAGTCTACGTGTGAGGTGAGGTGAGTGTGGGCTGGGTGTCGGAACAGG 452
Qy 121 AsnGlyThrArgLeuValValGluLysGluHisProGlnLeuGlyAlaGlyThrValLeu 140
Db 453 AATGGACCTGTGTTGGTGGAGAGGAGGACCTCTCAGCTAGCGGCTGGCACAGTCTCTC 512
Qy 141 LeuLeuArgAlaGlyPheTyrAlaValSerPheLeuSerValAlaValGlySerThrVal 160
Db 513 CTCCTCGGGCTGGATCTATGCCTTCAGCTTCTCTCGGTGCTATGGGCAGCAGCATG 572

RESULT 15

AW967444 719 bp mRNA linear EST 01-JUN-2000
LOCUS
DEFINITION EST379519 MAGE resequences, MAGJ Homo sapiens cDNA, mRNA sequence.
ACCESSION AW967444
VERSION AW967444.1 GI:8157281
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE

1 (bases 1 to 719)
Hegde, P., Qi, R., Abernathy, K., Dharap, S., Gaspard, R., Gay, C.,
Holt, I. E., Saeed, A. I., Sharov, V., Lee, N. H., Yeatman, T. J. and
Quackenbush, J.
Assessment of gene expression patterns in a model of colon tumor
metastasis using a 19,200 element cDNA microarray
Unpublished (2000)

TITLE

JOURNAL

COMMENT

Contact: John Quackenbush

The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 3528
Fax: 301 838 0208
Email: johnq@tigr.org
Plate: 241

Seq primer: Forward.

Location/Qualifiers

source
1..719
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="MAGE resequences, MAGJ"
/note="vector: pBluescriptSKm"

ORIGIN

Alignment Scores:
Pred. No.: 5,42e-48 Length: 719
Score: 620.00 Matches: 124
Percent Similarity: 87.0% Conservative: 3
Best Local Similarity: 84.9% Mismatches: 18
Query Match: 58.1% Indels: 1
DB: 1 Gaps: 0

US-10-696-259-6 (1-201) x AW967444 (1-719)

Qy 1 MetAlaTrpMetLeuLeuLeuLeuLeuMetValHisProGlySerCysAlaLeuTrp 20
Db 284 ATGGCTGGATGCTGTGTTGCTCATCTTGATCATGTCCATCCAGGATCTCTGTCTCTCGG 343
Qy 21 ValSerGlnProGluLeuLeuLeuLeuGluGlySerSerAlaPheLeuProCysSer 40
Db 344 GTGTCCAGCCCTCGAATCGTACCTCGAAGGATCTCTGTCTCTCTGCTCTGCTCTCC 403
Qy 41 PheAsnAlaSerGlnGlyArgLeuAlaIleGlySerValThrTrpPheArgAspGluVal 60
Db 404 TTCAATCCAGCCAGGAGACTGGCCATTTGGCTTCCTGTCACGTGGTTCGAGATGAGGGG 463
Qy 61 ValProGlyLysGluValArgAsnGlyThrProGluPheArgGlyArgLeuAlaProLeu 80
Db 464 GTTCCAGGAGGAGGTGAGGAATGGAACTCCAGAGTTCCAGGGGCCCTGGCCCACTT 523
Qy 81 AlaSerSerArgPheLeuHisAspHisGlnAlaGluLeuHisIleArgAspValArgGly 100
Db 524 GCTTCTTCCCGTTTCTCTCATGACCAACAGCTGAGCTGGACATTCCGGACGTCGAGGC 583
Qy 101 HisAspAlaSerIleTyrValCys-ArgValGluValLeuGlyLeuGlyThrGly 120
Db 584 CATGACCCAGCATTTTACCTGTGCAGAGTGGAGGGGCTTGGGCTTGGGGTCGGGACAGG 643
Qy 120 YAsnGlyThrArgLeuValValGluLysGluHisProGlnLeuGlyAlaGlyThrValLe 140
Db 644 GAATGGGAATTCGTGTGTGGGGGAAAGAACACCTCAACTAGGGGCTGGTTCAAGACT 703
Qy 140 uLeuLeuArgAlaGly 145
Db 704 TCCCGCTGCGGTGGA 719

Search completed: February 28, 2006, 10:13:48
Job time : 3882 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: February 28, 2006, 06:56:54 ; Search time 192 Seconds
(without alignments)
1860.885 Million cell updates/sec

Title: US-10-696-259-6

Perfect score: 1067

Sequence: 1 MAWMLLILILVHPGSCALW.....APLPPPCGSSAHLPPVPG 201

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Deiop 6.0 , Delext 7.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh
-Q=/abs/ABSSWEB_spool/US10696259/runat_27022006_123559_27221/app_query.fasta.1
-DB=Issued Patents_NA -qfmt=fastap -SUFFIX=p2n.rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-HOST=abs05h -USR=US10696259 @CGN 1.1.193 @runat_27022006_123559_27221
-NCPU=6 -ICPU=3 -NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV.TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents_NA.*

- 1: /cgn2_6/ptodata/1/ina/1 COMB.seq.*
- 2: /cgn2_6/ptodata/1/ina/5 COMB.seq.*
- 3: /cgn2_6/ptodata/1/ina/6A COMB.seq.*
- 4: /cgn2_6/ptodata/1/ina/6B COMB.seq.*
- 5: /cgn2_6/ptodata/1/ina/H COMB.seq.*
- 6: /cgn2_6/ptodata/1/ina/PCUS COMB.seq.*
- 7: /cgn2_6/ptodata/1/ina/PP COMB.seq.*
- 8: /cgn2_6/ptodata/1/ina/RE COMB.seq.*
- 9: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
c 1	773	72.4	5581	3	US-08-973-544-1
2	126.5	11.9	8100	3	US-09-949-016-13460
3	126.5	11.9	8100	3	US-09-949-016-13461
4	120	11.2	1108	3	US-09-949-016-1718
5	120	11.2	1108	3	US-09-949-016-1719
6	118.5	11.1	1313	3	US-09-949-016-5578
7	116.5	10.9	672	3	US-09-023-655-1242
8	116.5	10.9	672	3	US-09-949-016-731
9	116	10.9	700	3	US-09-311-784A-31

10	115	10.8	669	3	US-09-646-561-44	Sequence 44, Appl
c 11	115	10.8	669	3	US-09-646-561-45	Sequence 45, Appl
12	115	10.8	1856	3	US-09-646-561-41	Sequence 41, Appl
c 13	115	10.8	1856	3	US-09-646-561-43	Sequence 43, Appl
14	113.5	10.6	2220	3	US-10-104-047-1739	Sequence 1739, Ap
15	112	10.5	669	3	US-09-646-561-49	Sequence 49, Appl
c 16	112	10.5	669	3	US-09-646-561-50	Sequence 50, Appl
17	112	10.5	1883	3	US-09-646-561-46	Sequence 46, Appl
c 18	112	10.5	1883	3	US-09-646-561-48	Sequence 48, Appl
19	110.5	10.4	804	2	US-08-416-336-1	Sequence 1, Appli
20	110.5	10.4	2418	3	US-09-949-016-1694	Sequence 1694, Ap
21	110	10.3	561	2	US-08-067-884-13	Sequence 13, Appl
22	110	10.3	561	2	US-08-008-898-13	Sequence 13, Appl
23	110	10.3	561	2	US-08-459-818-13	Sequence 13, Appl
24	110	10.3	561	2	US-08-889-666-13	Sequence 13, Appl
25	110	10.3	561	2	US-08-465-078-13	Sequence 13, Appl
26	110	10.3	561	2	US-08-725-776-13	Sequence 13, Appl
27	110	10.3	561	2	US-08-488-062-13	Sequence 13, Appl
28	110	10.3	561	3	US-08-228-208A-13	Sequence 13, Appl
29	110	10.3	561	3	US-08-253-783-35	Sequence 35, Appl
30	110	10.3	561	3	US-09-454-651B-13	Sequence 13, Appl
31	110	10.3	561	6	PCT-US95-06726-35	Sequence 35, Appl
32	109	10.2	749	3	US-09-303-040-9	Sequence 9, Appli
33	109	10.2	805	3	US-09-620-312D-62	Sequence 62, Appl
34	109	10.2	938	3	US-09-828-995B-25	Sequence 25, Appl
c 35	109	10.2	938	3	US-09-828-995B-27	Sequence 27, Appl
36	109	10.2	4403765	3	US-09-103-840A-2	Sequence 2, Appli
37	109	10.2	4411529	3	US-09-103-840A-1	Sequence 1, Appli
38	108.5	10.2	1985	3	US-09-907-794A-212	Sequence 212, App
39	108.5	10.2	1985	3	US-09-905-125A-212	Sequence 212, App
40	108.5	10.2	1985	3	US-09-902-775A-212	Sequence 212, App
41	108.5	10.2	1985	3	US-09-906-700-212	Sequence 212, App
42	108.5	10.2	1985	3	US-09-903-603A-212	Sequence 212, App
43	108.5	10.2	1985	3	US-09-904-920A-212	Sequence 212, App
44	108.5	10.2	1985	3	US-09-909-064-212	Sequence 212, App
45	108.5	10.2	1985	3	US-09-905-381A-212	Sequence 212, App

ALIGNMENTS

RESULT 1
US-08-973-544-1/c
; Sequence 1, Application US/08973544
; Patent No. 6338950
; GENERAL INFORMATION:
; APPLICANT: WEISS, Elisabeth
; TITLE OF INVENTION: NEW IMMUNOREGULATORY PROTEIN LST-1
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIKAI DO, MARCELSTEIN, MURRAY & ORAM LLP
; STREET: 655 Fifteenth St., NW, Suite 300, G St. Lobby
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-5701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/973,544
; FILING DATE: 18-DEC-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT EP 96/02663
; FILING DATE: 20-JUN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95109511.6
; FILING DATE: 20-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95112201.9
; FILING DATE: 03-AUG-1995

ATTORNEY/AGENT INFORMATION:
NAME: Kitts, Monica Chin
REGISTRATION NUMBER: 36,105
REFERENCE/DOCKET NUMBER: P8341-7073
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 638-5000
TELEFAX: (202) 638-4810

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5581 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:

NAME/KEY: exon

LOCATION: 48..162

FEATURE:

NAME/KEY: exon

LOCATION: 544..652

FEATURE:

NAME/KEY: exon

LOCATION: 1044..1162

FEATURE:

NAME/KEY: exon

LOCATION: 1475..1567

FEATURE:

NAME/KEY: exon

LOCATION: 1775..1797

FEATURE:

NAME/KEY: exon

LOCATION: 2325..2709

US-08-973-544-1

Alignment Scores:

Pred. No.: 1,27e-71 Length: 5581
Score: 773.00 Matches: 181
Percent Similarity: 51.1% Conservative: 0
Best Local Similarity: 51.1% Mismatches: 4
Query Match: 72.4% Indels: 171
DB: 3 Gaps: 3

US-10-696-259-6 (1-201) x US-08-973-544-1 (1-5581)

Qy 16 SerCysAlaLeuTrpValSerGlnProGluLeuArgThrLeuGluGlySerSerAla 35
Db 3948 TCCTGTCTCTCTGGGTGTCCAGCCCTCAGATTCGTACCCCTGGAGGATCCTCTGCC 3889
Qy 36 PheLeuProCysSerPheAsnAlaSerGlnGlyArgLeuAlaIleGlySerValThrTrp 55
Db 3888 TTCTGTCCCTGCTCTCTCAATGCCAGCCAGGGAGACTGGCCATTTGGCTCCGTCACTGG 3829
Qy 56 PheArgAspGluValValProGlyLysGluValArgAsnGlyThrProGluPheArgGly 75
Db 3828 TTCCGAGATGAGTGGTTCCAGGAGGAGGTGAGGAATGAAACCCAGAGTTCCAGGGGC 3769
Qy 76 ArgLeuAlaProLeuAlaSerSerArgPheLeuHisAspHisGlnAlaGluLeuHisIle 95
Db 3768 GGCCT----CCATCTGCTTCTTCCCGTTTCTCCATGATGACCCAGGCTGAGCTGCACATC 3713
Qy 96 ArgAspValArgGlyHisAspAla-SerIleTyValCysArgValGluValLeuGlyLe 115
Db 3712 CGGACGTGCCAGGCCATGACCCAGGATCTTACGTGTGCAGATGGAGGTGTGGGCTT 3653
Qy 115 uGlyValGlyThrGlyAsnGlyThrArgLeuValValGluLys----- 129
Db 3652 TGGTGTCCGACAGGAATGGACTCGCTGGTGTGGAGAAAGTGTGAGATGCTGGGAGG 3593
Qy 129 ----- 129
Db 3592 TGGTGTCTCTCTGGTGGAGGCCAAGAGGCAATGTCTTTGGAGGACGAGGATGTCTCC 3533
Qy 129 ----- 129

Db 3532 TCTGAGGCCCTTCCCTCCCTGAGCCTGTGTGCACTTCTTCCCAACCCCGTCTCCATT 3473
Qy 130 -----GluHisProGlnLeu-GlyAlaGlyThrValLeuLeuLeuArgAlaGlyP 146
Db 3472 GCCCATGCAAGACATCCTCAGCTAGGGGCTGGTACAGTCTCCT-CTTCGGGCTGGAT 3414
Qy 146 heTyAlaValSerPheLeuSerValAlaValGlySerThrValTyTrGlnGlyLysC 166
Db 3413 TCTATGCTGTACGCTTCTCTGTGGCGTGGGACGACCGTCTATTACAGGGCAAT 3354
Qy 166 ys----- 166
Db 3353 GTGAGTAATGGACGAGGGCAATAGTGGACGGATGGGAGGGGACGTAAGAGAGTGGGA 3294
Qy 166 ----- 166
Db 3293 GGAGGGAGGACAGAGACAG 3234
Qy 166 ----- 166
Db 3233 GTCTCTCTGTGACGAGGCCACTGTTCACATGGGAACACACTGCCACTCTCAGATGGGCC 3174
Qy 166 ----- 166
Db 3173 CCGAGGAGTATTCCAGAGCCAGATGTCCCTAGTCTCTTTCAAAGAGACCCCAATAATC 3114
Qy 166 ----- 166
Db 3113 TGCCCCACCACTAACTCTCATGAGTCTCAAGTGTTCCTTCTTCCATTTCCAGATGCCA 3054
Qy 167 -----LeuThrTrp 169
Db 3053 AATCTACTCTCTCGGATTCCTCCCACTCTGAATTTCCCTTCCACAGGCTCTGACCTGG 2994
Qy 170 LysGlyProArgArgGlnLeuProAlaValValProAlaProLeuProProProCysGly 189
Db 2993 AAAGTCCAAAGAGGACGCTGCCGCTGTGGTCCAGCGCCCTCCCAACCATGTGGG 2934
Qy 190 SerSerAlaHisLeuLeuProProValProGlyGly 201
Db 2933 AGCTCAGCACATCTGCTTCCCGAGTCCCGAGGAGGC 2898

RESULT 2

US-09-949-016-13460
; Sequence 13460, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CU001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13460
; LENGTH: 8100
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-13460

Alignment Scores: 0.0129 Length: 8100
Pred. No.: 126.50 Matches: 64
Score: 38.9% Conservative: 20
Percent Similarity: 29.6% Mismatches: 82
Best Local Similarity:

Query Match: 11.9% Indels: 50
DB: 3 Gaps: 12

US-10-696-259-6 (1-201) x US-09-949-016-13460 (1-8100)

Qy 14 ProGlySerCysAlaLeuTrpValSerGln---ProProGluLeuAArgThrLeuGluGly 32
Db 3724 CCTGGGTGCAGGCCCTGTGGATGACAAAGGTCCCGCATCATTTGATGTGAGCCTGGGG 3783

Qy 33 SerSerAlaPheLeuProCysSerPheAsnAlaSerGlnGlyArgLeuAlaIleGlySer 52
Db 3784 GAAGAGCCCACTTCCAAATGCCCGCACATAGCAGCAACAC-----GCCAAC 3831

Qy 53 ValThrTrpPheArgAspGluValValProGlyLysGluValArgAsnGlyThr-----70
Db 3832 GTCACTGTGGTGGCC-----GTCTCCATGGC-----AATACACGTGGGCC 3873

Qy 71 ProGluPheArgGlyArgLeuAlaProLeuAlaSerSerArgPheLeuHisAspHisGln 90
Db 3874 CCTGAGTCTTGGGCCG-----GGCAGGAGCCCAAT 3906

Qy 91 AlaGluLeuHisIleArgAspValArgGlyHisAspAlaSerIleTyrValCysArgVal 110
Db 3907 GGTACGCTGATCATCCAGATGTGAACAGAGCCATGGGGCATATACGTGTGCCGGTGC 3966

Qy 111 GluValLeuGlyLeuGlyValGlyThrGlyAsnGlyThrArgLeuValValGluLysGlu 130
Db 3967 CAGGAGGGCAACAGATCATACAGAGCTCTCGGCGACCTACTCTCGGCTGGCGGTGAG 4026

Qy 131 HisProGlnLeuGly-----AlaGlyThrValLeuLeu-----141
Db 4027 TGGCCCGAGCCCTGGGCCCTTCTCCACTGTCCCGCTGGGGACACTCGGTTTATCTTGA 4086

Qy 142 -----LeuArgAlaGlyPheTyr-----AlaValSe 150
Db 4087 GTGGGATAGAGCCAGTACCTTCAATGTGGTTTCAACCGCTTGGACAGGAGCAGA 4146

Qy 150 rPheLeuSerValAlaValGlySerThrValTyrGlnGlyLysCysLeuThrTriPly 170
Db 4147 CATTCCTCTGCAGAGTGGGTCT---CTGGGGGTCTGGGGCTTGCAGGAGTGGGC 4203

Qy 170 sGlyPro-----ArgArgGlnLeuProAlaValValProAlaProLeuProPr 186
Db 4204 GGGGCCAGGAGGCTAGGGAGGCAAGAGGGCCAGGGCTC-----TGAGCCATACTACC 4257

Qy 186 oProCysGlySerSerAlaHisLeuLeuProValProGlyGly 201
Db 4258 TCCTTGAGAGCGCCGCCCGCCCTTCTTGACATGGGGGAGG 4303

RESULT 3

US-09-949-016-13461
; Sequence 13461, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13461
; LENGTH: 8100
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-13461

Best Local Similarity: 27.0% Mismatches: 93
 Query Match: 10.9% Indels: 29
 DB: 3 Gaps: 7

US-10-696-259-6 (1-201) x US-09-023-655-1242 (1-672)

QY 6 LeuLeuLeuLeuLeuMetValHisProGlySerCys---AlaLeuTrpValSerGlnPro 24
 Db 70 CTCCTGTTTTCTCTCTTCATCCCTGCTCTGCAAGCAATGACGCGCCAGCCT 129
 QY 25 ProGluLeuArgThrLeuGluGlySerSerAlaPheLeuProCysSerPheAsnAlaSer 44
 Db 130 GCTGTGTACTGCGCCAGCAGCGAGGCATCGCCAGCTTTGTGTGAGTAT---GCACT 186
 QY 45 GlnGlyArgLeuAlaIleGlySerValThrTrpPheArgAspGluValProGlyLys 64
 Db 187 CAGGCAAGCCACTAGGTCGCGGTGACAGTGCTTCGCGCAGGCTGACAGCGAGTGACT 246
 QY 65 GluValArgAsnGlyThrProGluPheArgGlyArgLeuAlaProLeuAlaSerSerArg 84
 Db 247 GAACTCTGTGCGCAACCTACATGACGGGGAGTGTGACC----- 288
 QY 85 PheLeuHisAsp-----HisGlnAlaGluLeuHisIle 95
 Db 289 TTCCTAGATGATTCATCTGCACGGGCACCTCCAGTGGAAATCAAGTGAACCTCACTATC 348
 QY 96 ArgAspValArgGlyHisAspAlaSerIleTyrValCysArgValGluValLeu----- 113
 Db 349 CAAGGACTAGGGCCATGACAGGGACCTCTACATCTGCAAGTGGAGCTCATGTACCA 408
 QY 114 ---GlyLeuGlyValGlyThrGlyAsnGlyThrArgLeuValValGluLysGluHisPro 132
 Db 409 CGCCATACCTAGTGGCATAGCAACGCAACCCAGATTATGTAATTGATCCAGAACCG 468
 QY 133 GlnLeuGlyAlaGlyThrValLeuLeuLeuArgAla-----GlyPheTyrAla 148
 Db 469 TGCCAGATCTGACTTCCTCTCGGATCCTTGACGAGTGTAGTTCGGGGTGTGTTTT 528
 QY 149 ValSerPheLeuSerValAlaValGlySerThrValTyrTyrGlnGlyLysCysLeuThr 168
 Db 529 TATAGCTTCTCTCACAGCTGTTCTTTGAGC-----AAATGCTAAAG 573
 QY 169 TrpLysGlyProArgArgGlnLeuProAlaValProAlaProLeuProProCys 188
 Db 574 AAAAGAAGCCCTTTACACAGGGGTCTATGTGAAATGCCCCCAACAGACGCAAGATGT 633

RESULT 8

US-09-949-016-731
 ; Sequence 731, Application US/09949016
 ; Patent No. 6812339
 ; GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig et al.
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 ; FILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: CL001307
 ; CURRENT APPLICATION NUMBER: US/09/949,016
 ; CURRENT FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: 60/241,755
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/237,768
 ; PRIOR FILING DATE: 2000-10-03
 ; PRIOR APPLICATION NUMBER: 60/231,498
 ; PRIOR FILING DATE: 2000-09-08
 ; NUMBER OF SEQ ID NOS: 207012
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 731
 ; LENGTH: 672
 ; TYPE: DNA
 ; ORGANISM: Human
 US-09-949-016-731

Alignment Scores:

Pred. No.: 0.00404 Length: 672

Score: 116.50 Matches: 54
 Percent Similarity: 39.0% Conservative: 24
 Best Local Similarity: 27.0% Mismatches: 93
 Query Match: 10.9% Indels: 29
 DB: 3 Gaps: 7

US-10-696-259-6 (1-201) x US-09-949-016-731 (1-672)

QY 6 LeuLeuLeuLeuLeuMetValHisProGlySerCys---AlaLeuTrpValSerGlnPro 24
 Db 70 CTCCTGTTTTCTCTCTTCATCCCTGCTCTGCAAGCAATGACGCGCCAGCCT 129
 QY 25 ProGluLeuArgThrLeuGluGlySerSerAlaPheLeuProCysSerPheAsnAlaSer 44
 Db 130 GCTGTGTACTGCGCCAGCAGCGAGGCATCGCCAGCTTTGTGTGAGTAT---GCACT 186
 QY 45 GlnGlyArgLeuAlaIleGlySerValThrTrpPheArgAspGluValProGlyLys 64
 Db 187 CAGGCAAGCCACTAGGTCGCGGTGACAGTGCTTCGCGCAGGCTGACAGCGAGTGACT 246
 QY 65 GluValArgAsnGlyThrProGluPheArgGlyArgLeuAlaProLeuAlaSerSerArg 84
 Db 247 GAACTCTGTGCGCAACCTACATGACGGGGAGTGTGACC----- 288
 QY 85 PheLeuHisAsp-----HisGlnAlaGluLeuHisIle 95
 Db 289 TTCCTAGATGATTCATCTGCACGGGCACCTCCAGTGGAAATCAAGTGAACCTCACTATC 348
 QY 96 ArgAspValArgGlyHisAspAlaSerIleTyrValCysArgValGluValLeu----- 113
 Db 349 CAAGGACTAGGGCCATGACAGGGACCTCTACATCTGCAAGTGGAGCTCATGTACCA 408
 QY 114 ---GlyLeuGlyValGlyThrGlyAsnGlyThrArgLeuValValGluLysGluHisPro 132
 Db 409 CGCCATACCTAGTGGCATAGCAACGCAACCCAGATTATGTAATTGATCCAGAACCG 468
 QY 133 GlnLeuGlyAlaGlyThrValLeuLeuLeuArgAla-----GlyPheTyrAla 148
 Db 469 TGCCAGATCTGACTTCCTCTCGGATCCTTGACGAGTGTAGTTCGGGGTGTGTTTT 528
 QY 149 ValSerPheLeuSerValAlaValGlySerThrValTyrTyrGlnGlyLysCysLeuThr 168
 Db 529 TATAGCTTCTCTCACAGCTGTTCTTTGAGC-----AAATGCTAAAG 573
 QY 169 TrpLysGlyProArgArgGlnLeuProAlaValProAlaProLeuProProCys 188
 Db 574 AAAAGAAGCCCTTTACACAGGGGTCTATGTGAAATGCCCCCAACAGACGCAAGATGT 633

RESULT 9

US-09-311-784A-31
 ; Sequence 31, Application US/09311784A
 ; Patent No. 6534482
 ; GENERAL INFORMATION:
 ; APPLICANT: Fikes, John D.
 ; APPLICANT: Hermanson, Gary G.
 ; APPLICANT: Sette, Alessandro
 ; APPLICANT: Ishioka, Glenn Y.
 ; APPLICANT: Livingston, Brian
 ; APPLICANT: Chesnut, Robert W.
 ; APPLICANT: Epimmune Inc.
 ; TITLE OF INVENTION: Expression Vectors for Stimulating an
 ; FILE OF INVENTION: Immune Response and Methods of Using the Same
 ; FILE REFERENCE: 39963-20022.01
 ; CURRENT APPLICATION NUMBER: US/09/311,784A
 ; CURRENT FILING DATE: 1999-05-13
 ; PRIOR APPLICATION NUMBER: 1999-05-13
 ; PRIOR FILING DATE: 1998-05-15
 ; NUMBER OF SEQ ID NOS: 463
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 31
 ; LENGTH: 700
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens

; PRIOR APPLICATION NUMBER: 09/062,597
 ; PRIOR FILING DATE: 1998-04-17
 ; NUMBER OF SEQ ID NOS: 65
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 45
 ; LENGTH: 669
 ; TYPE: DNA
 ; ORGANISM: Canis familiaris
 US-09-646-561-45

Alignment Scores:
 Pred. No.: 0.00579 Length: 669
 Score: 115.00 Matches: 53
 Percent Similarity: 42.7% Conservative: 32
 Best Local Similarity: 26.6% Mismatches: 97
 Query Match: 10.8% Indels: 28
 DB: 3 Gaps: 7

US-10-696-259-6 (1-201) x US-09-646-561-45 (1-669)

```

QY 6 LeuLeuLeuLeuMetValHisProGlySerCysAlaLeuTrpValSerGlnProPro 25
Db 597 CTGTTTCTCTCTCTTTATCCCGGTCTTCCAAAGGGATGCATGGCTCAGCCTGCA 538
QY 26 GluLeuArgThrLeuGluGlySerSerAlaPheLeuProCysSerPhe----- 41
Db 537 GTGGTCTCGCCAGCAGCGGGGTGTGCTAGCTTGGTGCTGATATGGGTCTTCAGGC 478
QY 42 AsnAlaSerGlnGlyArgLeuAlaIleGlySerValThrTrpPheArgAspGluVal 61
Db 477 AACGACGCGAGGTCCGGGTGCACAGTGCT-CCGCGAGGCTGGCAGCCAGATGACTGA 419
QY 62 ProGlyLysGluValArgAsnGlyThrProGluPheArgGlyArgLeuAlaProLeu 81
Db 418 CTGTGCCCGACATACACAGTGG-----GGATGAGTGGC---CTTCCT 377
QY 82 SerSerArgPheLeuHisAspHis-----GlnAlaGluLeuHisIleArgAsp 97
Db 376 GGATGATTCTACCTGCACCGGCACCTCCAGTGGAAACAAAGTGAACCTCACCATCCA 317
QY 98 ValArgGlyHis-AspAlaSerIleTyrValCysArgValGluValLeu----- 114
Db 316 GTTAGGCGCCATGACACGCGGCTCTACATCTGCAAGTGGAGTGCATGTACCCACCACC 257
QY 114 YLeuGlyValGlyThrGlyAsnGlyThrArgLeuValValGluLysGluHisProGln 134
Db 256 CTACTATGTAGCATGGGAATGGAACCCAGATTATGTCTATCGATCTGAACTTGCCTCC 197
QY 134 uGlyAlaGlyThrValLeuLeuLeuArgAla-----GlyPheTyrAlaValSe 150
Db 196 AGATTCTGACTTCCTCTCTGATCTTGCAGCAGTCAGTTCGGGCTTGTGTTTTATAG 137
QY 150 rPheLeuSerValAlaValGlySerThrValTyrTyrGlnGlyLysCysLeuThrTrp 170
Db 136 CTTTCTTATCACAGCTGTTCTTTGAGC-----AAATGCTAAAGAAAG 92
QY 170 sGlyProArgGlnLeuProAlaValProAlaProLeuProProCys 188
Db 91 AAGCCCTCTTACCACAGGGGTCTATGTGAAATGCCCCCACTGAGCCAGAAATGT 37
  
```

RESULT 12

US-09-646-561-41
 ; Sequence 41, Application US/09646561
 ; Patent No. 6852847
 ; GENERAL INFORMATION:
 ; APPLICANT: Yang, Shumin
 ; APPLICANT: Sim, Gek-Kee
 ; APPLICANT: Sellins, Karen S.
 ; TITLE OF INVENTION: NOVEL FORMS OF T CELL COSTIMULATORY PROTEINS, NUCLEIC
 ; FILE REFERENCE: IN-1-C1-PCT
 ; CURRENT APPLICATION NUMBER: US/09/646,561
 ; CURRENT FILING DATE: 2000-09-19

; PRIOR APPLICATION NUMBER: 60/078,765
 ; PRIOR FILING DATE: 1998-03-19
 ; PRIOR APPLICATION NUMBER: 09/062,597
 ; PRIOR FILING DATE: 1998-04-17
 ; NUMBER OF SEQ ID NOS: 65
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 41
 ; LENGTH: 1856
 ; TYPE: DNA
 ; ORGANISM: Canis familiaris
 ; NAME/KEY: CDS
 ; LOCATION: (60)..(731)
 US-09-646-561-41

Alignment Scores:
 Pred. No.: 0.0255 Length: 1856
 Score: 115.00 Matches: 53
 Percent Similarity: 42.7% Conservative: 32
 Best Local Similarity: 26.6% Mismatches: 87
 Query Match: 10.8% Indels: 28
 DB: 3 Gaps: 7

US-10-696-259-6 (1-201) x US-09-646-561-41 (1-1856)

```

QY 6 LeuLeuLeuLeuMetValHisProGlySerCysAlaLeuTrpValSerGlnProPro 25
Db 132 CTGTTTCTCTCTCTTTATCCCGGTCTTCCAAAGGGATGCATGGCTCAGCCTGCA 191
QY 26 GluLeuArgThrLeuGluGlySerSerAlaPheLeuProCysSerPhe----- 41
Db 192 GTGGTCTCGCCAGCAGCGGGGTGTGCTAGCTTGGTGCTGATATGGGTCTTCAGGC 251
QY 42 AsnAlaSerGlnGlyArgLeuAlaIleGlySerValThrTrpPheArgAspGluVal 61
Db 252 AACGACGCGAGGTCCGGGTGCACAGTGCT-CCGCGAGGCTGGCAGCCAGATGACTGA 310
QY 62 ProGlyLysGluValArgAsnGlyThrProGluPheArgGlyArgLeuAlaProLeu 81
Db 311 CTGTGCCCGACATACACAGTGG-----GGATGAGTGGC---CTTCCT 352
QY 82 SerSerArgPheLeuHisAspHis-----GlnAlaGluLeuHisIleArgAsp 97
Db 353 GGATGATTCTACCTGCACCGGCACCTCCAGTGGAAACAAAGTGAACCTCACCATCCA 412
QY 98 ValArgGlyHis-AspAlaSerIleTyrValCysArgValGluValLeu----- 114
Db 413 GTTAGGCGCCATGACACGCGGCTCTACATCTGCAAGTGGAGTGCATGTACCCACCACC 472
QY 114 YLeuGlyValGlyThrGlyAsnGlyThrArgLeuValValGluLysGluHisProGln 134
Db 473 CTACTATGTAGCATGGGAATGGAACCCAGATTATGTCTGATCTTCACTGATCTTGA 532
QY 134 uGlyAlaGlyThrValLeuLeuLeuArgAla-----GlyPheTyrAlaValSe 150
Db 533 AGATTCTGACTTCCTCTCTGATCTTGCAGCAGTCAGTTCGGGCTTGTGTTTTATAG 592
QY 150 rPheLeuSerValAlaValGlySerThrValTyrTyrGlnGlyLysCysLeuThrTrp 170
Db 593 CTTTCTTATCACAGCTGTTCTTTGAGC-----AAATGCTAAAGAAAG 637
QY 170 sGlyProArgGlnLeuProAlaValProAlaProLeuProProCys 188
Db 638 AAGCCCTCTTACCACAGGGGTCTATGTGAAATGCCCCCACTGAGCCAGAAATGT 692
  
```

RESULT 13

US-09-646-561-43/c
 ; Sequence 43, Application US/09646561
 ; Patent No. 6852847
 ; GENERAL INFORMATION:
 ; APPLICANT: Sim, Gek-Kee
 ; APPLICANT: Yang, Shumin
 ; APPLICANT: Sellins, Karen S.

```
; TITLE OF INVENTION: NOVEL FORMS OF T CELL COSTIMULATORY PROTEINS, NUCLEIC
; FILE REFERENCE: ACID MOLECULES, AND USES THEREOF
; CURRENT APPLICATION NUMBER: US/09/646,561
; PRIOR FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: 60/078,765
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 09/062,597
; PRIOR FILING DATE: 1998-04-17
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 43
; LENGTH: 1856
; TYPE: DNA
; ORGANISM: Canis familiaris
US-09-646-561-43

Alignment Scores:
Pred. No.: 0.0255 Length: 1856
Score: 115.00 Matches: 53
Percent Similarity: 42.7% Conservative: 32
Best Local Similarity: 26.6% Mismatches: 87
Query Match: 10.8% Indels: 28
DB: 3 Gaps: 7

US-10-696-259-6 (1-201) x US-09-646-561-43 (1-1856)

Qy 6 LeuLeuIleLeuIleMetValHisProGlySerCysAlaLeuTrpValSerGlnProPro 25
Db 1725 CTGTTTCTCTCTCTTATCCCGCTTCTTCAAAGGATGATGGCTCAGCCTGCA 1666

Qy 26 GluIleAArgThrLeuGluGlySerSerAlaPheLeuProCysSerPhe----- 41
Db 1665 GTGGTTCTGGCCAGCAGCGGGGTGTGCTAGCTTCTGTGTGAATATGGTCTTCAGGC 1606

Qy 42 AsnAlaSerGlnGlyArgLeuAlaIleGlySerValThrTrpPheArgAspGluValVal 61
Db 1605 AACGACGCCAGGTCGCGGTGCACAGTGTCT-GCGGACGGCTGGCAGCCAGATGACTGAAGT 1547

Qy 62 ProGlyLysGluValArgAsnGlyThrProGluPheArgGlyArgLeuAlaProLeuAla 81
Db 1546 CTGTGCCCGGACATACACAGTGA-----GGATGAGTTGGC---CTTCCT 1505

Qy 82 SerSerArgPheLeuHisAspHis-----GlnAlaGluLeuHisIleArgAsp 97
Db 1504 GGATGATTCACCTGCACCGGCACCTCCAGTGGAAACAAAGTGAACCTCACCATCCAAGG 1445

Qy 98 ValArgGlyHis-AspAlaSerIleTyrValCysArgValGluValLeu-----G1 114
Db 1444 GTTGAGGGCCATGACACCGGGGCTCTACATCTGCAAGGTGGAGCTCATGTACCCACCACC 1385

Qy 114 YLeuGlyValGlyThrGlyAenGlyThrArgLeuValValGluLysGluHisProGlnLe 134
Db 1384 CTACTATGTAGGCATGGAAATGAACCCAGATTATGTATCATGCATCTGAAACCTGCC 1325

Qy 134 uGlyAlaGlyThrValLeuLeuLeuArgAla-----GlyPheTyrAlaValSe 150
Db 1324 AGATTCGACTTCTCTCTCTGATCCTTGACAGCAGTCAGTTCGGGCTGTTTTTATAG 1265

Qy 150 rPheLeuSerValAlaValGlySerThrValTyrGlnGlyLysCysLeuThrTrpLy 170
Db 1264 CTTTCTTATCACAGCTGTTCTTTGAGC-----AAAATGCTAAAGAAAAG 1220

Qy 170 sGlyProArgGlnLeuProAlaValProAlaProLeuProProProCys 188
Db 1219 AAGCCCTCTTACCACAGGGGTCTATGTGAAATAATGCCCACTGAGCCAGAATGT 1165

RESULT 14
US-10-104-047-1739
; Sequence 1739, Application US/10104047
; Patent No. 6943241
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE.
```

```
; TITLE OF INVENTION: No. 6943241el full length cDNA
; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; PRIOR FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1739
; LENGTH: 2220
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-104-047-1739

Alignment Scores:
Pred. No.: 0.0477 Length: 2220
Score: 113.50 Matches: 50
Percent Similarity: 37.4% Conservative: 18
Best Local Similarity: 27.5% Mismatches: 72
Query Match: 10.6% Indels: 42
DB: 3 Gaps: 7

US-10-696-259-6 (1-201) x US-10-104-047-1739 (1-2220)

Qy 15 GlySerCysAlaLeuTrpValSerGlnPro-----ProGluIle 27
Db 707 GGGAAAGACGGCGGTGGTGTGCAAGTCCACCAAGTATGAGATGGCCTCCACAGACCTG 766

Qy 28 ArgThrLeuGluGlySerSerAlaPheLeuProCysSerPheAsnAlaSerGlnGlyArg 47
Db 767 TCCACCACCAAGAGCTCCACGCTTCTTGCTTGAAGCGGAGGGGCACTCTCTAG- 823

Qy 48 LeuAlaIleGlySerValThrTrpPheArgAspGluValValProGlyLysGluValArg 67
Db 824 -----CCCAACATCACCTGGGACAAAGAT----- 847

Qy 68 AsnGlyThrProGluPheArgGlyArgLeuAlaProLeuAlaSerSerArgPheLeuHis 87
Db 848 -----GGCCAGCTGTGTGGGGCGCCGAGGGGAAAGTTCCACCATC 886

Qy 88 AspHisGlnAlaGluLeuHisIleArgAspValArgGlyHisAspAlaSerIleTyrVal 107
Db 887 CAGCCTTCTGGGAGTGTGTGTGAAGAACTTGGAGGGCCAGGACGACCATATACC 946

Qy 108 CysArgValGlu---ValLeuGlyLeuGlyValGlyThrGlyAenGlyThrArgLeuVal 126
Db 947 TGTACCGCTGAGAACCGCGTGGGCGCGGCGCGGCGGTGCACCTCACCATCTCTGGTA 1006

Qy 127 ValGluLys-GluHisProGlnLeuGly---AlaGlyThrValLeuLeuLeuArgAlaG1 145
Db 1007 CTGCTGTGTTCACCACTCTGCTGGGGACCGCAGCTGGCGCTTGGGGACAGGCTGTGG 1066

Qy 145 yPhe-----TyrAlaValSerPheLeuSerValAlaVal 156
Db 1067 CTTTCGTGTGCACCGCGGGGACGCCACCCCTCGCATTTGGCTGGAGCTGTCAACGACCGG 1126

Qy 156 lGlySerThrValTyrGlnGlyLysCysLeuThrTrpLysGlyProArgGlnLe 176
Db 1127 CCAGTCACAGTCTGGGTC-----TGCTGGCATGGGTGGGACAGAGCCAGGCAC 1177

Qy 176 uPro 177
Db 1178 ACCG 1181

RESULT 15
US-09-646-561-49
; Sequence 49, Application US/09646561
; Patent No. 6852847
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Kee
; APPLICANT: Yang, Shumin
; APPLICANT: Sellins, Karen S.
; TITLE OF INVENTION: NOVEL FORMS OF T CELL COSTIMULATORY PROTEINS, NUCLEIC
```

/ TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF

/ FILE REFERENCE: IM-1-CI-PCT

/ CURRENT APPLICATION NUMBER: US/09/646,561

/ PRIOR FILING DATE: 2000-09-19

/ PRIOR APPLICATION NUMBER: 60/078,765

/ PRIOR FILING DATE: 1998-03-19

/ PRIOR APPLICATION NUMBER: 09/062,597

/ PRIOR FILING DATE: 1998-04-17

/ NUMBER OF SEQ ID NOS: 65

/ SOFTWARE: PatentIn Ver. 2.0

/ SEQ ID NO 49

/ LENGTH: 669

/ TYPE: DNA

/ ORGANISM: Felis catus

US-09-646-561-49

Alignment Scores:

Pred. No.:	0.0121	Length:	669
Score:	112.00	Matches:	52
Percent Similarity:	38.2%	Conservative:	24
Best Local Similarity:	26.1%	Mismatches:	95
Query Match:	10.5%	Indels:	28
DB:	3	Gaps:	6

US-10-696-259-6 (1-201) x US-09-646-561-49 (1-669)

QY	6	LeuLeuIleLeuIleMetValHisProGlySerCysAlaLeuTrpValSerGlnProPro	25
Db	73	CTGTTTTCTCTCTCTTTATCCCCGCTCTTCCAAAGGAGTCATGTGGCCAGCCTGCA	132
QY	26	GlulIleArgThrLeuGluGlySerSerAlaPheLeuProCysSerPheAsnAlaSerGln	45
Db	133	GTGGTGTGGCCAGCAGCGAGGTGTCGCCAGCTCGTGTGTGAATATGGGTCTTCA---	189
QY	46	GlyArgLeuAlaIleGlySerValThrTrpPheArgSerGluValValProGlyLysGlu	65
Db	190	GGCAATGCCGCCGAAGTCCGAGTCTGTGTGAGGCGAGACTGGCGAGCCAGATGACTGAA	249
QY	66	ValArgAsnGlyThrProGluPheArgGlyArgLeuAlaProLeuAlaSerSerArgPhe	85
Db	250	GTCTGTGTGGCAGACATACACAGTGGAGATGAGTTGGCC-----TTC	291
QY	86	LeuHisAsp-----HisGlnAlaGluLeuHisIleArg	96
Db	292	CTAGATGATTCACCTGTCACCTGGCATCTCCAGCGGAAACAAAGTGAACCTCACCATCAA	351
QY	97	AspValArgGlyHisAspAlaSerIleTyrValCysArgValGluValLeu-----	113
Db	352	GGGTGAGGGCCATGGACACGGGACTCTACATCTGCAAGTGGAGCTCATGTACCCACCA	411
QY	114	GlyLeuGlyValGlyThrGlyAsnGlyThrArgLeuValValGluLysGluHisProGln	133
Db	412	CCCTACTATGCAGGCATGGCAATGGAACCCAGATTATGTTCATCGATCCTGAACTTGC	471
QY	134	LeuGlyAlaGlyThrValLeuLeuArgAla-----GlyPheTyrAlaVal	149
Db	472	CCAGATTCGACTCTCTCTCTGATCTCCAGCAGCTAGTTCAGGATTGTTTTTTAT	531
QY	150	SerPheLeuSerValAlaValGlySerThrValTyrTyrGlnGlyLysCysLeuThrTip	169
Db	532	AGCTTCTTATCAGCTGTTCTTTTGAGC-----AAATGCTAAAGAAA	576
QY	170	LysGlyProArgArgGlnLeuProAlaValProAlaProLeuProProProCys	188
Db	577	AGAAGCCCTCTTACTACAGGGGTCTATGTGAAATGCCCAACAGAGCCAGATGT	633

Search completed: February 28, 2006, 07:19:18

Job time : 203 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: February 28, 2006, 07:04:48 ; Search time 775 Seconds
(without alignments)
2144.703 Million cell updates/sec

Title: US-10-696-259-6

Perfect score: 1067

Sequence: 1 MAMLLILIMVHPCALW.....APLPCCGSSAHLPPVPGG 201

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh
-Q=/abs/ABSSWEB_spool/US10696259/runat_27022006_123601_27279/app_query.fasta_1
-DB=Published Applications_NA_Main -QMT=fastcap -SUFFIX=p2n.rnpbm
-MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1
-MATRIX=blosum62 -TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct
-THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext
-HEAPSIZE=500 -MILEN=0 -MAXLEN=2000000000 -HOST=abes03h
-USER=US10696259 @CGN_1_1_1026 @runat_27022006_123601_27279 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -USFBILOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA_Main:

1: /cgn2_6/ptodata/1/pubna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubna/US08_PUBCOMB.seq:*
3: /cgn2_6/ptodata/1/pubna/US09A_PUBCOMB.seq:*
4: /cgn2_6/ptodata/1/pubna/US09B_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubna/US10A_PUBCOMB.seq:*
6: /cgn2_6/ptodata/1/pubna/US10B_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubna/US10C_PUBCOMB.seq:*
8: /cgn2_6/ptodata/1/pubna/US10D_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubna/US10E_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1067	100.0	1061	9	US-10-895-225A-31
2	1039	97.4	834	7	US-10-696-259-3
3	997	93.4	889	7	US-10-696-259-2
4	876	82.1	573	5	US-10-036-444-13
5	876	82.1	573	10	US-11-137-649-13
6	876	82.1	606	5	US-10-036-444-12
7	876	82.1	606	10	US-11-137-649-12

8	876	82.1	674	5	US-10-036-444-1	Sequence 1, Appli
9	876	82.1	674	10	US-11-137-649-1	Sequence 1, Appli
10	872	81.7	22173	7	US-10-322-696-28	Sequence 28, Appl
11	848	79.5	671	7	US-10-696-259-1	Sequence 1, Appli
12	773	72.4	5581	2	US-08-973-444-1	Sequence 1, Appli
13	728	68.2	421	5	US-10-036-444-10	Sequence 10, Appl
14	728	68.2	421	10	US-11-137-649-10	Sequence 10, Appl
15	713	66.8	405	7	US-10-333-481-15	Sequence 15, Appl
16	713	66.8	1110	7	US-10-333-481-16	Sequence 16, Appl
17	464.5	43.5	3673778	6	US-10-312-841-1	Sequence 1, Appli
18	440	41.2	3673778	6	US-10-312-841-2	Sequence 2, Appli
19	225.5	21.1	21781	7	US-10-322-696-25	Sequence 25, Appl
20	131.5	12.3	967	5	US-10-158-646-74	Sequence 74, Appl
21	126.5	11.9	44075	3	US-09-997-722-40	Sequence 40, Appl
22	125.5	11.8	869	3	US-09-909-567B-13	Sequence 13, Appl
23	125	11.7	636	3	US-09-898-195A-16	Sequence 16, Appl
24	125	11.7	636	5	US-10-057-288-11	Sequence 11, Appl
25	125	11.7	636	5	US-10-155-514-1	Sequence 1, Appli
26	125	11.7	636	7	US-10-419-008-16	Sequence 16, Appl
27	125	11.7	636	8	US-10-742-564A-5	Sequence 5, Appli
28	125	11.7	636	9	US-10-740-645A-5	Sequence 5, Appli
29	125	11.7	636	9	US-10-910-531-16	Sequence 16, Appl
30	125	11.7	11265	5	US-10-185-318-1	Sequence 1, Appli
31	125	11.7	11265	5	US-10-185-799-1	Sequence 1, Appli
32	122	11.4	1483	5	US-10-161-572-25	Sequence 25, Appl
33	122	11.4	1530	3	US-09-766-511B-32	Sequence 32, Appl
34	122	11.4	1533	3	US-09-972-268-32	Sequence 32, Appl
35	122	11.4	1533	7	US-10-058-270A-53	Sequence 53, Appl
36	122	11.4	1558	5	US-10-161-572-24	Sequence 24, Appl
37	122	11.4	2642	5	US-10-161-572-23	Sequence 23, Appl
38	122	11.4	2680	6	US-10-295-027-65	Sequence 65, Appl
39	122	11.4	2680	6	US-10-173-999-75	Sequence 75, Appl
40	122	11.4	2680	7	US-10-188-832-178	Sequence 178, App
41	122	11.4	3389	7	US-10-422-571-14	Sequence 14, Appl
42	122	11.4	3389	7	US-10-422-571-111	Sequence 111, App
43	122	11.4	3389	7	US-10-422-571-113	Sequence 113, App
44	122	11.4	3401	7	US-10-422-571-16	Sequence 16, Appl
45	122	11.4	3401	7	US-10-422-571-117	Sequence 117, App

ALIGNMENTS

RESULT 1
US-10-895-225A-31
; Sequence 31, Application US/10895225A
; Publication No. US20050048587A1
; GENERAL INFORMATION:
; APPLICANT: Rao, Patricia
; APPLICANT: Snyder, Jessica
; APPLICANT: Bagley, Andria
; TITLE OF INVENTION: METHODS FOR IDENTIFYING TOLERANCE
; TITLE OF INVENTION: MODULATORY COMPOUNDS AND USES THEREFOR
; FILE REFERENCE: TUN-025
; CURRENT APPLICATION NUMBER: US/10/895,225A
; CURRENT FILING DATE: 2004-07-19
; PRIOR APPLICATION NUMBER: 60/498,502
; PRIOR FILING DATE: 2003-07-17
; NUMBER OF SEQ ID NOS: 161
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 1061
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-895-225A-31

Alignment Scores:
Pred. No.: 2.02e-115 Length: 1061
Score: 1067.00 Matches: 201
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 9 Gaps: 0

US-10-696-259-6 (1-201) x US-10-895-225A-31 (1-1061)

Qy 1 MetAlaTrpMetLeuLeuLeuLeuLeuLeuMetValHisProGlySerCysAlaLeuTrp 20
Db 265 ATGGCCCTGGATGCTGTGCTCATCTTATCATGATGCTCATCCAGGATCCTGTGCTCTCTGG 324
Qy 21 ValSerGlnProProGluLeuLeuArgThrLeuGluGlySerSerAlaPheLeuProCysSer 40
Db 325 GTGTCCCGAGCCCTCGAGATTCGTACCTTGAAGGATCCTCTGCTTCTGCTGCTGCTCC 384
Qy 41 PheAsnAlaSerGlnGlyArgLeuAlaLeuGlySerValThrTrpPheArgAspGluVal 60
Db 385 TTCAATGCCAGCCAGGAGAGACTGGCCATTGGCTCCGTCACGTGGTTCGAGATGAGGTG 444
Qy 61 ValProGlyLysGluValArgAsnGlyThrProGluPheArgGlyArgLeuAlaProLeu 80
Db 445 GTTCAGGGAAGGAGGTGAGGAATGGAACCCAGATTGAGGGCCGCTGGCCCCACTT 504
Qy 81 AlaSerSerArgPheLeuHisAspHisGlnAlaGluLeuHisIleArgAspValArgGly 100
Db 505 GCTTCTTCCCGTTTCTCCATGACCACCGCTGAGCTGCACATCCGGGAGCTGCGAGGC 564
Qy 101 HisAspAlaSerIleTyrValCysArgValGluValLeuGlyLeuGlyValGlyThrGly 120
Db 565 CATGACGCCAGCATCTACGTGTGCAGAGTGGAGGTGCTGGGCCCTTGGTGTGCGGACAGGG 624
Qy 121 AsnGlyThrArgLeuValValGluLysGluHisProGlnLeuGlyAlaGlyThrValLeu 140
Db 625 AATGGGACTCGCTGGTGGTGGAGAAAGAAATCCTCAGCTAGGGGCTGGTACAGTCCCTC 684
Qy 141 LeuLeuArgAlaGlyPheTyrAlaValSerPheLeuSerValAlaValAlaGlySerThrVal 160
Db 685 CTCCTTCGGGCTGGATTCTATGCTGTGAGCTTCTCTGTGGCGGTGGGAGCACCGTC 744
Qy 161 TyrTyrGlnGlyLysCysLeuThrTrpLysGlyProArgGlnLeuProAlaValVal 180
Db 745 TATTACGAGGCAATGTCTGACCTGGAAAGGTCCAAAGAGCGAGCTGCCGCTGTGGTC 804
Qy 181 ProAlaProLeuProProCysGlySerSerAlaHisLeuLeuProProValProGly 200
Db 805 CCAGCGCCCTCCACCACCATGTGGGAGCTCAGACATCTGCTTCCCCAGTCCCGAGGA 864
Qy 201 Gly 201
Db 865 GGC 867

RESULT 2

US-10-696-259-3
; Sequence 3, Application US/10696259
; Publication No. US20040110218A1
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC
; APPLICANT: BROWNING, Jeffrey
; TITLE OF INVENTION: BMOG, A Novel Protein Member of the
; TITLE OF INVENTION: Myelin-Oligodendrocyte Glycoprotein Family and Its Use for
; TITLE OF INVENTION: Immunomodulatory Purposes
; FILE REFERENCE: A041 US
; CURRENT APPLICATION NUMBER: US/10/696,259
; CURRENT FILING DATE: 2003-10-28
; PRIOR APPLICATION NUMBER: US/09/560,855A
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: PCT/US98/23826
; PRIOR FILING DATE: 1998-11-05
; PRIOR APPLICATION NUMBER: 60/064761
; PRIOR FILING DATE: 1997-11-07
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 834
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-696-259-3

Alignment Scores:

Pred. No.: 2 98e-112 Length: 834
Score: 1039.00 Matches: 200
Percent Similarity: 99.5% Conservative: 0
Best Local Similarity: 99.5% Mismatches: 1
Query Match: 97.4% Indels: 1
DB: 7 Gaps: 0

US-10-696-259-6 (1-201) x US-10-696-259-3 (1-834)

Qy 1 MetAlaTrpMetLeuLeuLeuLeuLeuMetValHisProGlySerCysAlaLeuTrp 20
Db 66 ATGGCCCTGGATGCTGTGCTCATCTTATCATGATGCTCATCCAGGATCCTGTGCTCTCTGG 125
Qy 21 ValSerGlnProProGluLeuLeuArgThrLeuGluGlySerSerAlaPheLeuProCysSer 40
Db 126 GTGTCCCGAGCCCTCGAGATTCGTACCTTGAAGGATCCTCTGCTTCTGCTGCTGCTCC 185
Qy 41 PheAsnAlaSerGlnGlyArgLeuAlaLeuGlySerValThrTrpPheArgAspGluVal 60
Db 186 TTCAATGCCAGCCAGGAGACTGGCCATTGGCTCCGTCACGTGGTTCGAGATGAGGTG 245
Qy 61 ValProGlyLysGluValArgAsnGlyThrProGluPheArgGlyArgLeuAlaProLeu 80
Db 246 GTTCAGGGAAGGAGGTGAGGAATGGAACCCAGATTGAG-GGGCGCTGGCCCCACTT 304
Qy 81 AlaSerSerArgPheLeuHisAspHisGlnAlaGluLeuHisIleArgAspValArgGly 100
Db 305 GCTTCTTCCCGTTTCTCCATGACCACCGCTGAGCTGCACATCCGGGAGCTGCGAGGC 364
Qy 101 HisAspAlaSerIleTyrValCysArgValGluValLeuGlyLeuGlyValGlyThrGly 120
Db 365 CATGACGCCAGCATCTACGTGTGCAGAGTGGAGGTGCTGGCCCTTGGTGTGCGGACAGGG 424
Qy 121 AsnGlyThrArgLeuValValGluLysGluHisProGlnLeuGlyAlaGlyThrValLeu 140
Db 425 AATGGGACTCGCTGGTGGTGGAGAAAGAAATCCTCAGCTAGGGGCTGGTACAGTCCCTC 484
Qy 141 LeuLeuArgAlaGlyPheTyrAlaValSerPheLeuSerValAlaValAlaGlySerThrVal 160
Db 485 CTCCTTCGGGCTGGATTCTATGCTGTGAGCTTCTCTGTGGCGGTGGGAGCACCGTC 544
Qy 161 TyrTyrGlnGlyLysCysLeuThrTrpLysGlyProArgArgGlnLeuProAlaValVal 180
Db 545 TATTACGAGGCAATGTCTGACCTGGAAAGGTCCAAAGAGCGAGCTGCCGCTGTGGTC 604
Qy 181 ProAlaProLeuProProCysGlySerSerAlaHisLeuLeuProProValProGly 200
Db 605 CCAGCGCCCTCCACCACCATGTGGGAGCTCAGACATCTGCTTCCCCAGTCCCGAGGA 664
Qy 201 Gly 201
Db 665 GGC 667

RESULT 3
US-10-696-259-2
; Sequence 2, Application US/10696259
; Publication No. US20040110218A1
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC
; APPLICANT: BROWNING, Jeffrey
; TITLE OF INVENTION: BMOG, A Novel Protein Member of the
; TITLE OF INVENTION: Myelin-Oligodendrocyte Glycoprotein Family and Its Use for
; TITLE OF INVENTION: Immunomodulatory Purposes
; FILE REFERENCE: A041 US
; CURRENT APPLICATION NUMBER: US/10/696,259
; CURRENT FILING DATE: 2003-10-28
; PRIOR APPLICATION NUMBER: US/09/560,855A
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: PCT/US98/23826
; PRIOR FILING DATE: 1998-11-05
; PRIOR APPLICATION NUMBER: 60/064761
; PRIOR FILING DATE: 1997-11-07

```

; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 889
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-696-259-2

Alignment Scores:
Pred. No.:      2,88e-107    Length:      889
Score:          997.00       Matches:     199
Percent Similarity: 90.5%   Conservative: 0
Best Local Similarity: 90.5% Mismatches:    2
Query Match:     93.4%      Indels:       20
DB:              Gaps:        7

US-10-696-259-6 (1-201) x US-10-696-259-2 (1-889)

Qy 1 MetAlaTrpMetLeuLeuLeuLeuLeuLeuMetValHisProGlySerCysAlaLeuTrp 20
Db 66 ATGGCTCGATGCTGTTCATCTTGCATCATGTCATCCAGGATCCTGTCTCTCTGG 125

Qy 21 ValSerGlnProGluLeuArgThrLeuGluGlySerSerAlaPheLeuProCysSer 40
Db 126 GTGTCCAGCCCCCTGAGATTGTTACCTTGGAAGATCTCTGTCTCTGCTCTCTCC 185

Qy 41 PheAsnAlaSerGlnGlyArgLeuAlaIleGlySerValThrTrpPheArgAspGluVal 60
Db 186 TTCAATGCCAGGCCAAGGAGACTGGCCATTGGCTCGTCACGTGGTTCGAGATGAGTG 245

Qy 61 ValProGlyLysGluValArgAnGlyThrProGluPheArgGlyArgLeuAlaProLeu 80
Db 246 GTTCCAGGAAAGAGAGTGAAGAATGGAACCCAGAGTTTCAG-GGGCGCCTGGCCCCACTT 304

Qy 81 AlaSerSerArgPheLeuHisAspHisGlnAlaGluLeuHisIleArgAspValArgGly 100
Db 305 GCCTCTTCCTGCTTCTCCATGACCACAGGCTGAGCTGCACATCCGGACGTGGAGGC 364

Qy 101 HisAspAlaSerIleTyrrValCysArgValGluValLeuGlyLysValGlyThrGly 120
Db 365 CATGACGCCAGCATCTACGTGTCGAGAGTGAGGTGCTGGGCTTGGTTCGGGACAGG 424

Qy 121 AsnGlyThrArgLeuValValGluLysGluHisProGlnLeuGlyAlaGlyThrValLeu 140
Db 425 AATGGGACTCGGCTGGTGGTGGAGAAAGAACAATCCTCAGTAGGGGCTGGTACAGTCCTC 484

Qy 141 LeuLeuArgAlaGlyPheTyrrAlaValSerPheLeuSerValAlaValGlySerThrVal 160
Db 485 CTCCTTCGGGCTGGATTCATGCTGTGACGTTTCTCTCTGTGGCCGTGGGACGACCGTC 544

Qy 161 TyrrTyrrGlnGlyLys-Cys----- 166
Db 545 TATTACCAGGGCAAATATGCCAAATCTACTCTCTCGGATTCCTCCCACTCTGAATTC 604

Qy 167 -----LeuThrTriplysGlyProArgArgGlnLeuProAlaValProAl 182
Db 605 CCTTCCACCAGGTCTCACCTCGGAAGGTCCTCAAGAGGAGGTCGCGGCTGGTCCCAGC 664

Qy 182 aProLeuProProProCysGlySerSerAlaHisIleLeuLeuProValProGlyGly 201
Db 665 GCCCTTCCCACCACCATGTGGGAGCTCAGACATCTGTCTTCTTCCCCCAGTCCCGAGGAG 722

RESULT 4
US-10-036-444-13
; Sequence 13, Application US/10036444
; Publication No. US20020142445A1
; GENERAL INFORMATION:
; APPLICANT: INNATE PHARMA S.A.S.
; APPLICANT: UNIVERSITA DI GENOVA
; TITLE OF INVENTION: "No. US20020142445A1el triggering receptor involved in natural
; TITLE OF INVENTION: cytotoxicity mediated by human Natural Killer cells and
; FILE REFERENCE: SEQ-FR-1060

CURRENT APPLICATION NUMBER: US/10/036,444
; CURRENT FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: 09/440,514
; PRIOR FILING DATE: 1999-11-15
; PRIOR APPLICATION NUMBER: 09/456,199
; PRIOR FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 573
; TYPE: DNA
; ORGANISM: Human NK cell
US-10-036-444-13

Alignment Scores:
Pred. No.:      3,01e-93    Length:      573
Score:          876.00       Matches:     173
Percent Similarity: 90.2%   Conservative: 2
Best Local Similarity: 89.2% Mismatches:    7
Query Match:     82.1%      Indels:     12
DB:              Gaps:        5

US-10-696-259-6 (1-201) x US-10-036-444-13 (1-573)

Qy 1 MetAlaTrpMetLeuLeuLeuLeuLeuMetValHisProGlySerCysAlaLeuTrp 20
Db 1 ATGGCTCGATGCTGTTCATCTTGCATCATGTCATCCAGGATCCTGTCTCTCTCTGG 60

Qy 21 ValSerGlnProGluLeuArgThrLeuGluGlySerSerAlaPheLeuProCysSer 40
Db 61 GTGTCCAGCCCCCTGAGATTGTCCTGGGAAGGATCTCTGTCTCTCTGCTCTCTCTC 120

Qy 41 PheAsnAlaSerGlnGlyArgLeuAlaIleGlySerValThrTrpPheArgAspGluVal 60
Db 121 TTCAATGCCAGGCCAAGGAGACTGGCCATTGGCTCTCCTCAGTGGTTCGAGATGAGTG 180

Qy 61 ValProGlyLysGluValArgAnGlyThrProGluPheArgGlyArgLeuAlaProLeu 80
Db 181 GTTCCAGGAAAGAGAGTGAAGAATGGAACCCAGAGTTTCAGGGCGCCTGGCCCCACTT 240

Qy 81 AlaSerSerArgPheLeuHisAspHisGlnAlaGluLeuHisIleArgAspValArgGly 100
Db 241 GCCTTCTTCCTGCTTCTCCATGACCACAGGCTGAGCTGCACATCCGGACGTGGCAGGC 300

Qy 101 HisAspAlaSerIleTyrrValCysArgValGluValLeuGlyLysValGlyThrGly 120
Db 301 CATGACGCCAGCATCTACGTGTCGACAGTGGAGGTGCTGGGCTTGGTGTGGGACAGG 360

Qy 121 AsnGlyThrArgLeuValValGluLysGluHisProGlnLeuGlyAlaGlyThrValLeu 140
Db 361 AATGGGACTCGGCTGGTGGTGGAGAAAGAACAATCCTCAGTAGGGGCTGGTACAGTCCTC 420

Qy 141 LeuLeuArgAlaGlyPheTyrrAlaValSerPheLeuSerValAlaValGlySerThrVal 160
Db 421 CTCTTTCGGGCTGGATTCATGCTGTGACGTTTCTCTGTGGCCGTGGGACGACCGTC 480

Qy 161 TyrrTyrrGlnGlyLys-----CysLeuThrTriplysGlyPro 172
Db 481 TATTACCAGGGCAAATGCCCACTGTCTACATGGGNAACACACTGCCACTCTCCTCAGATGGGCC 540

Qy 173 ArgArgGlnLeuProAlaValValProAlaProLeuProPro 186
Db 541 CGA-----GGRGTGATTCCAGAGCCCATGATGTCCC 570

RESULT 5
US-11-137-649-13
; Sequence 13, Application US/11137649
; Publication No. US20050221438A1
; GENERAL INFORMATION:
; APPLICANT: INNATE PHARMA S.A.S.
; APPLICANT: UNIVERSITA DI GENOVA
; TITLE OF INVENTION: "Novel triggering receptor involved in natural
; TITLE OF INVENTION: cytotoxicity mediated by human Natural Killer cells and
; FILE REFERENCE: SEQ-FR-1060

```

; TITLE OF INVENTION: antibodies that identify the same"

; FILE REFERENCE: SEQ-PR-1060
; CURRENT APPLICATION NUMBER: US/11/137,649
; PRIOR FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US/10/036,444
; PRIOR FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: 09/440,514
; PRIOR FILING DATE: 1999-11-15
; PRIOR APPLICATION NUMBER: 09/456,199
; PRIOR FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 573
; TYPE: DNA
; ORGANISM: Human NK cell
US-11-137-649-13

Alignment Scores:
Pred. No.: 3,01e-93 Length: 573
Score: 876.00 Matches: 173
Percent Similarity: 90.2% Conservativeness: 2
Best Local Similarity: 89.2% Mismatches: 7
Query Match: 82.1% Indels: 12
DB: 10 Gaps: 2

US-10-696-259-6 (1-201) x US-11-137-649-13 (1-573)

QY 1 MetAlaTrpMetLeuLeuLeuLeuLeuLeuMetValHisProGlySerCysAlaLeuTrp 20
Db 1 ATGGCTGTGATGCTGTGCTCATCTTGATCATGTCATCCAGGATCTGTGCTCTGG 60
QY 21 ValSerGlnProGluLeuLeuLeuLeuLeuGluGlySerSerAlaPheLeuProCysSer 40
Db 61 GTGTCCAGCCCTCAGATTCGTACCTCTGGAGGATCTCTGCTCTCTGCTCTCTCC 120
QY 41 PheAsnAlaSerGlnGlyArgLeuAlaLeuLeuLeuLeuLeuLeuLeuLeuVal 60
Db 121 TTCAATGCCAGCAAGGAGAGCTGGCCATTTGGCTCCGTCACTGCTGCTGCTGCTG 180
QY 61 ValProGlyLysGluValArgAsnGlyThrProGluPheArgGlyValArgLeuAlaProLeu 80
Db 181 GTTCCAGGAGAGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAG 240
QY 81 AlaSerSerArgPheLeuHisAspHisGlnAlaGluLeuHisIleArgAspValArgGly 100
Db 241 GCTTCTCCCGTTCTCTCATGACCAACAGGCTGAGCTGCATCCGGGCGCTGGCCACTT 300
QY 101 HisAspAlaSerIleTyrValCysArgValGluValLeuGlyLeuGlyValGlyThrGly 120
Db 301 CATGACGCCAGCATCTACGTGTGCAGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAG 360
QY 121 AsnGlyThrArgLeuValValGluLysGluHisProGlnLeuGlyAlaGlyThrValLeu 140
Db 361 AATGGGACTCGCTGGTGGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
QY 141 LeuLeuArgAlaGlyPheTyrAlaValSerPheLeuSerValAlaValGlySerThrVal 160
Db 421 CTCTCTCGGGTGGATTCTATGCTGTCTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGT 480
QY 161 TyrTyrGlnGlyLys-----CysLeuThrTrpLysGlyPro 172
Db 481 TATTACAGGCAAAATGCTCATATGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGT 540
QY 173 ArgArgGlnLeuProAlaValProAlaProLeuProPro 186
Db 541 CGA-----GGRGTGATTCCAGAGCCAGAGATGTCCC 570

RESULT 6

US-10-036-444-12
; Sequence 12, Application US/10036444
; Publication No. US2002014245A1
; GENERAL INFORMATION:

; APPLICANT: INNATE PHARMA S.A.S.

; APPLICANT: UNIVERSITA DI GENOVA

; TITLE OF INVENTION: "No. US2002014245A1e1 triggering receptor involved in natural
; TITLE OF INVENTION: cytotoxicity mediated by human Natural Killer cells and
; TITLE OF INVENTION: antibodies that identify the same"

; FILE REFERENCE: SEQ-PR-1060

; CURRENT APPLICATION NUMBER: US/10/036,444

; CURRENT FILING DATE: 2002-01-07

; PRIOR APPLICATION NUMBER: 09/440,514

; PRIOR FILING DATE: 1999-11-15

; PRIOR APPLICATION NUMBER: 09/456,199

; PRIOR FILING DATE: 1999-12-07

; NUMBER OF SEQ ID NOS: 13

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 12

; LENGTH: 606

; TYPE: DNA

; ORGANISM: Human NK cell

US-10-036-444-12

Alignment Scores:

Pred. No.: 3.23e-93 Length: 606
Score: 876.00 Matches: 173
Percent Similarity: 90.2% Conservativeness: 2
Best Local Similarity: 89.2% Mismatches: 7
Query Match: 82.1% Indels: 12
DB: 5 Gaps: 2

US-10-696-259-6 (1-201) x US-10-036-444-12 (1-606)

QY 1 MetAlaTrpMetLeuLeuLeuLeuLeuLeuMetValHisProGlySerCysAlaLeuTrp 20
Db 8 ATGGCTGTGATGCTGTGCTCATCTTGATCATGTCATCCAGGATCTGTGCTCTGG 67
QY 21 ValSerGlnProGluLeuLeuLeuLeuLeuGluGlySerSerAlaPheLeuProCysSer 40
Db 68 GTGTCCAGCCCTCAGATTCGTACCTCTGGAGGATCTCTGCTCTCTGCTCTCTCC 127
QY 41 PheAsnAlaSerGlnGlyArgLeuAlaLeuLeuLeuLeuLeuLeuLeuLeuVal 60
Db 128 TTCAATGCCAGCAAGGAGAGCTGGCCATTTGGCTCCGTCACTGCTGCTGCTGCTG 187
QY 61 ValProGlyLysGluValArgAsnGlyThrProGluPheArgGlyValArgLeuAlaProLeu 80
Db 188 GTTCCAGGAGAGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAG 247
QY 81 AlaSerSerArgPheLeuHisAspHisGlnAlaGluLeuHisIleArgAspValArgGly 100
Db 248 GCTTCTCCCGTTCTCTCATGACCAACAGGCTGAGCTGCATCCGGGCGCTGGCCACTT 307
QY 101 HisAspAlaSerIleTyrValCysArgValGluValLeuGlyLeuGlyValGlyThrGly 120
Db 308 CATGACGCCAGCATCTACGTGTGCAGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAG 367
QY 121 AsnGlyThrArgLeuValValGluLysGluHisProGlnLeuGlyAlaGlyThrValLeu 140
Db 368 AATGGGACTCGCTGGTGGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 427
QY 141 LeuLeuArgAlaGlyPheTyrAlaValSerPheLeuSerValAlaValGlySerThrVal 160
Db 428 CTCTCTCGGGTGGATTCTATGCTGTCTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGT 487
QY 161 TyrTyrGlnGlyLys-----CysLeuThrTrpLysGlyPro 172
Db 488 TATTACAGGCAAAATGCTCATATGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGT 547
QY 173 ArgArgGlnLeuProAlaValProAlaProLeuProPro 186
Db 548 CGA-----GGRGTGATTCCAGAGCCAGAGATGTCCC 577

RESULT 7

US-11-137-649-12
; Sequence 12, Application US/11137649

Publication No. US20050221438A1
; GENERAL INFORMATION:
; APPLICANT: INNATE PHARMA S.A.S.
; TITLE OF INVENTION: "Novel triggering receptor involved in natural
; TITLE OF INVENTION: cytotoxicity mediated by human Natural Killer cells and
; TITLE OF INVENTION: antibodies that identify the same"
; FILE REFERENCE: SEQ-PR-1060
; CURRENT APPLICATION NUMBER: US/11/337,649
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US/10/036,444
; PRIOR FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: 09/440,514
; PRIOR FILING DATE: 1999-11-15
; PRIOR APPLICATION NUMBER: 09/456,199
; PRIOR FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 606
; TYPE: DNA
; ORGANISM: Human NK cell
US-11-137-649-12

Alignment Scores:
Pred. No.: 3,23e-93 Length: 606
Score: 876.00 Matches: 173
Percent Similarity: 90.2% Conservative: 2
Best Local Similarity: 89.2% Mismatches: 7
Query Match: 82.1% Indels: 12
DB: 10 Gaps: 2

US-10-696-259-6 (1-201) x US-11-137-649-12 (1-606)

Qy 1 MetAlaTrpMetLeuLeuLeuLeuLeuLeuMetValHisProGlySerCysAlaLeuTrp 20
Db 8 ATGGCCCTGGATGCTGTGCTCATCTTGATCATGGTCCATCCAGGATCTGTGCTCTCGG 67
Qy 21 ValSerGlnProProGluIleArgThrLeuGluGlySerSerAlaPheLeuProCysSer 40
Db 68 GTGTCCACAGCCCTGAGATTGCTACCTCGAAGGATCTCTGCTTCTGCTCCCTGCTCC 127
Qy 41 PheAsnAlaSerGlnGlyArgLeuAlaIleGlySerValThrTrpPheArgAspGluVal 60
Db 128 TTCAATGCCAGCAAGGAGACTGGCCATTGGCTCCGTCACGTGGTCCGAGATCAGGTG 187
Qy 61 ValProGlyLysGluValArgAsnGlyThrProGluPheArgGlyArgLeuAlaProLeu 80
Db 188 GTTCCAGGAAGGAGGTGAGAAATGGAAACCCAGAGTTTCAGGGGCGGCTGGCCCACTT 247
Qy 81 AlaSerSerArgPheLeuHisAspHisGlnAlaGluLeuHisIleArgAspValArgGly 100
Db 248 GCTTCTCCGTTTCTCCATGACCAACAGGCTGAGCTGCATCCGGGAGCTGCGAGGC 307
Qy 101 HisAspAlaSerIleTyrValCysArgValGluValLeuGlyLeuGlyValGlyThrGly 120
Db 308 CATGACGCGACATCTACGTGTGCAGAGTGGAGGTGCTGGGCCCTTGGTGTGCGGACAGG 367
Qy 121 AsnGlyThrArgLeuValValGluLysGluHisProGlnLeuGlyAlaGlyThrValLeu 140
Db 368 AATCGGACTCGGCTGGTGGTGGAGAAAGAAATCATCTCAGCTAGGGGCTGGTACAGTCCCTC 427
Qy 141 LeuLeuArgAlaGlyPheTyrAlaValSerPheLeuSerValAlaValGlySerThrVal 160
Db 428 CTCCTTCGGGCTGGAATCTATGCTGTACGCTTCTCTGTGGCGGTGGGAGCAGCCGTC 487
Qy 161 TyrTyrGlnGlyLys-----CysLeuThrTrpLysGlyPro 172
Db 488 TATTACAGGGCAAAATGCCACTGTGCATGGGAACACACTGCCACTCTCAGATGGGCC 547
Qy 173 ArgArgGlnLeuProAlaValValProAlaProLeuProPro 186
Db 548 CGA-----GGRGTTATCCAGAGCCAGATGTCCC 577

RESULT 8
US-10-036-444-1
; Sequence 1, Application US/10036444
; Publication No. US20020142445A1
; GENERAL INFORMATION:
; APPLICANT: INNATE PHARMA S.A.S.
; APPLICANT: UNIVERSITA DI GENOVA
; TITLE OF INVENTION: "No. US20020142445A1el triggering receptor involved in natural
; TITLE OF INVENTION: cytotoxicity mediated by human Natural Killer cells and
; TITLE OF INVENTION: antibodies that identify the same"
; FILE REFERENCE: SEQ-PR-1060
; CURRENT APPLICATION NUMBER: US/10/036,444
; CURRENT FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: 09/440,514
; PRIOR FILING DATE: 1999-11-15
; PRIOR APPLICATION NUMBER: 09/456,199
; PRIOR FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 674
; TYPE: DNA
; ORGANISM: Human NK cell
US-10-036-444-1

Alignment Scores:
Pred. No.: 3,69e-93 Length: 674
Score: 876.00 Matches: 173
Percent Similarity: 90.2% Conservative: 2
Best Local Similarity: 89.2% Mismatches: 7
Query Match: 82.1% Indels: 12
DB: 5 Gaps: 2

US-10-696-259-6 (1-201) x US-10-036-444-1 (1-674)

Qy 1 MetAlaTrpMetLeuLeuLeuLeuLeuMetValHisProGlySerCysAlaLeuTrp 20
Db 64 ATGGCCCTGGATGCTGTGCTCATCTTGATCATGGTCCATCCAGGATCTGTGCTCTCGG 123
Qy 21 ValSerGlnProProGluIleArgThrLeuGluGlySerSerAlaPheLeuProCysSer 40
Db 124 GTGTCCACAGCCCTGAGATTGCTACCTCGAAGGATCTCTGCTTCTGCTCCCTGCTCC 183
Qy 41 PheAsnAlaSerGlnGlyArgLeuAlaIleGlySerValThrTrpPheArgAspGluVal 60
Db 184 TTCAATGCCAGCAAGGAGACTGGCCATTGGCTCCGTCACGTGGTCCGAGATCAGGTG 243
Qy 61 ValProGlyLysGluValArgAsnGlyThrProGluPheArgGlyArgLeuAlaProLeu 80
Db 244 GTTCCAGGAAGGAGGTGAGAAATGGAAACCCAGAGTTTCAGGGGCGGCTGGCCCACTT 303
Qy 81 AlaSerSerArgPheLeuHisAspHisGlnAlaGluLeuHisIleArgAspValArgGly 100
Db 304 GCTTCTCCGTTTCTCCATGACCAACAGGCTGAGCTGCATCCGGGAGCTGCGAGGC 363
Qy 101 HisAspAlaSerIleTyrValCysArgValGluValLeuGlyLeuGlyValGlyThrGly 120
Db 364 CATGACGCGACATCTACGTGTGCAGAGTGGAGGTGCTGGGCCCTTGGTGTGCGGACAGG 423
Qy 121 AsnGlyThrArgLeuValValGluLysGluHisProGlnLeuGlyAlaGlyThrValLeu 140
Db 424 AATGGGACTCGGCTGGTGGTGGAGAAAGAAATCATCTCAGCTAGGGGCTGGTACAGTCCCTC 483
Qy 141 LeuLeuArgAlaGlyPheTyrAlaValSerPheLeuSerValAlaValGlySerThrVal 160
Db 484 CTCCTTCGGGCTGGAATCTATGCTGTACGCTTCTCTGTGGCGGTGGGAGCAGCCGTC 543
Qy 161 TyrTyrGlnGlyLys-----CysLeuThrTrpLysGlyPro 172
Db 544 TATTACAGGGCAAAATGCCACTGTGCATGGGAACACACTGCCACTCTCAGATGGGCC 603
Qy 173 ArgArgGlnLeuProAlaValValProAlaProLeuProPro 186

```
|||||
Db 604 CGA-----GGRGTGATTCAGAGCCAGCATGTCCC 633
|||||
RESULT 9
US-11-137-649-1
; Sequence 1, Application US/11137649
; Publication No. US20050221438A1
; GENERAL INFORMATION:
; APPLICANT: INNATE PHARMA S.A.S.
; APPLICANT: UNIVERSITA DI GENOVA
; TITLE OF INVENTION: "Novel triggering receptor involved in natural
; TITLE OF INVENTION: cytotoxicity mediated by human Natural Killer cells and
; TITLE OF INVENTION: antibodies that identify the same"
; FILE REFERENCE: SEQ-PR-1060
; CURRENT APPLICATION NUMBER: US/11/137,649
; CURRENT FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US/10/036,444
; PRIOR FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: 09/440,514
; PRIOR FILING DATE: 1999-11-15
; PRIOR APPLICATION NUMBER: 09/456,199
; PRIOR FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 674
; TYPE: DNA
; ORGANISM: Human NK cell
US-11-137-649-1
Alignment Scores:
Pred. No.: 3,69e-93 Length: 674
Score: 876.00 Matches: 173
Percent Similarity: 50.2% Conservative: 2
Best Local Similarity: 89.2% Mismatches: 7
Query Match: 82.1% Indels: 12
DB: 10 Gaps: 2
US-10-696-259-6 (1-201) x US-11-137-649-1 (1-674)
Qy 1 MetAlaTrpMetLeuLeuLeuLeuLeuLeuMetValHisProGlySerCysAlaLeuTrp 20
Db 64 ATGGCTCGATGCTGCTCTCATCTTGATCATGTGTCATCCAGGATCTGTGCTCTCTGG 123
Qy 21 ValSerGlnProGluLeuLeuLeuLeuLeuLeuGlySerSerAlaPheLeuProCysSer 40
Db 124 GTGTCCTCCAGCCCTGAGATTTCGATTCCTGGAAGGATCTCTGCTCTCTGCTGCTCC 183
Qy 41 PheAsnAlaSerGlnGlyArgLeuAlaLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuVal 60
Db 184 TTCAATGCCAGCCAGGAGAGACTGGCCATTGGCTCCGTCAGTGGTCCGAGATGAGGTG 243
Qy 61 ValProGlyLysGluValArgAsnGlyThrProGluPheArgGlyArgLeuAlaProLeu 80
Db 244 GTTCAGGGAAGGAGGTGAGGAATGGAACCCAGAGTTTCAGGGCCGCTGGCCCTT 303
Qy 81 AlaSerSerArgPheLeuHisAspHisGlnAlaGluLeuHisIleArgAspValArgGly 100
Db 304 GCTTCTTCCCTTCCCTCATGACACACAGGCTGAGTGCACATCCCGGAGCTGCGAGGC 363
Qy 101 HisAspAlaSerIleTyrValCysArgValGluValLeuLeuGlyLeuGlyValGlyThrGly 120
Db 364 CATGACGCCAGCATCATGCTGTCAGAGTGGAGGTGCTGGGCTTGGTGTGCGACAGGG 423
Qy 121 AsnGlyThrArgLeuValValGluLysGluHisProGlnLeuGlyAlaGlyThrValLeu 140
Db 424 AATGGGACTCGGCTGGTGGTGAGAAAGAAACATCTCTCAGCTAGGGGCTGGTACAGTCTC 483
Qy 141 LeuLeuArgAlaGlyPheTyrAlaValSerPheLeuSerValAlaValGlySerThrVal 160
Db 484 CTCCTTGGGGTGATTTCTATGCTGTACGTTTCTCTGTGGCCGTGGGAGCAGCCGTC 543
Qy 161 TyrTyrGlnGlyLys-----CysLeuThrTrpLysGlyPro 172
|||||
Db 544 TATTACCAGGGCAAAATGCCACTGTTCACATGGGAACACACTGCCACTCTCTCAGATGGGCC 603
|||||
Qy 173 ArgArgGlnLeuProAlaValValProAlaProLeuProPro 186
|||||
Db 604 CGA-----GGRGTGATTCAGAGCCAGCATGTCCC 633
|||||
RESULT 10
US-10-322-696-28
; Sequence 28, Application US/10322696
; Publication No. US20040166490A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Malandro, Marc
; TITLE OF INVENTION: NOVEL THERAPEUTIC TARGETS IN CANCER
; FILE REFERENCE: 529452001200
; CURRENT APPLICATION NUMBER: US/10/322,696
; CURRENT FILING DATE: 2003-10-17
; NUMBER OF SEQ ID NOS: 186
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 22173
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-322-696-28
Alignment Scores:
Pred. No.: 8,92e-91 Length: 22173
Score: 872.00 Matches: 191
Percent Similarity: 52.5% Conservative: 1
Best Local Similarity: 52.2% Mismatches: 2
Query Match: 81.7% Indels: 172
DB: 7 Gaps: 3
US-10-696-259-6 (1-201) x US-10-322-696-28 (1-22173)
Qy 3 TrpMetLeuLeuLeuLeuLeuLeuMetValHisProGlySerCysAlaLeuTrpValSer 22
Db 2577 TGGGTCTTCTCTCTG-----CCCCAGGATCTCTGTCTCTGGGTGTCC 2621
Qy 23 GlnProGluLeuLeuLeuLeuLeuGlySerValHisProGlySerAlaPheLeuProCysSerPheAsn 42
Db 2622 CAGCCCCCTCAGATTCGTACCTCTGGAAGGATCTCTGCTCTCTGCTCTCTCTCAAT 2681
Qy 43 AlaSerGlnGlyArgLeuAlaLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuValPro 62
Db 2682 GCAGCCCAAGGAGACTGGCCATTGGCTCGCTACGCTGGTTCGAGATGAGGTGTCCA 2741
Qy 63 GlyLysGluValArgAsnGlyThrProGluPheArgGlyArgLeuAlaProLeuAlaSer 82
Db 2742 GGGAGAGGTGAGGAATGGAAACCCAGAGTTTCAGGGCCGCTGGCCCTCTGCTTCT 2801
Qy 83 SerArgPheLeuHisAspHisGlnAlaGluLeuHisIleArgAspValArgGlyHisAsp 102
Db 2802 TCCGCTTCTCTCATGACCACAGGCTGAGTGCACATCCGAGCTGCGAGGCCATGAC 2861
Qy 103 AlaSerIleTyrValCysArgValGluValLeuLeuGlyLeuGlyValGlyThrGlyHisAsnGly 122
Db 2862 GCCAGCATCTACGCTGTGACAGTGGAGTGGAGTGGTGGTGGTGGTGGTGGTGGTGGTGG 2921
Qy 123 ThrArgLeuValValGluLys----- 129
Db 2922 ACTCGGCTGGTGGTGGAGAAAGGTGAGATGCTGGAGAGGTGTCTCTCTCTCTCTCTCTCTCT 2981
Qy 129 ----- 129
Db 2982 GCCCAAGAGGCAATGCTCTTGGAGGAGGATGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 3041
Qy 130 -----GluHisProGly 133
Db 3042 GAGCCTGTGTGCACTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 3101
Qy 133 nLeuGlyAlaGlyThrValLeuLeuLeuLeuArgAlaGlyPheTyrAlaValSerPheLeuSe 153
```

```
Db 3102 GCTAGGGGCTGGTACAGTCCCTCTCGGGCTGGATTCTATGCTGTCAGCTTTCTCTC 3161
Qy 153 rValAlaValGlySerThrValTyrTyrGlnGlyLysCys----- 166
Db 3162 TGTGGCGTGGGAGCACCCTCTATTACCAAGGCAATGTGAGTAATGGAGCCAGGGGCA 3221
Qy 166 ----- 166
Db 3222 ATAGTGGACGGGATGGGAGGGCAGTAAGAGAGTGGGAGGAGGAGACAGACCAGGA 3281
Qy 166 ----- 166
Db 3282 AGAGGAGAGCCTCGGGAAGTCAACACTGAGCAGCTCTCTCTCTCTGTGACCAGGCCAC 3341
Qy 166 ----- 166
Db 3342 TGTACATGGGAACACACTGCCACTCTCTCAGATGGGCCCCGAGGAGTGATTCAGAGCCC 3401
Qy 166 ----- 166
Db 3402 AGATGTCCTAGTCTCTTCAAAAGAGCCCCAATAAATCTGCCCCACCACTAACTCTCAT 3461
Qy 166 ----- 166
Db 3462 GAGTCTCAAGTGTCTTCTTCTCCATTCTCCAGATGCCAAATCTACTCTCTCCGGATTCCC 3521
Qy 167 -----LeuThrTyrLysGlyProArgArgGlnLeup 177
Db 3522 CCAACTCTGAATCTTCCCTCCACAGGCTCTGACTGGAAGGTCGAAGAGGAGGAGCTGC 3581
Qy 177 roAlaValProAlaProLeuProProCysGlySerSerAlaHisLeuLeuProp 197
Db 3582 CGGCTGTGGTCCAGCGCCCTCCACACCACCATGTGGAGCTCAGCACATCTGCTTCCCC 3641
Qy 197 roValProGlyGly 201
Db 3642 CAGTCCAGGAGGC 3655
```

RESULT 11

```
US-10-696-259-1
; Sequence 1, Application US/10696259
; Publication No. US20040110218A1
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC
; TITLE OF INVENTION: BMOG, A Novel Protein Member of the
; TITLE OF INVENTION: Myelin-Oligodendrocyte Glycoprotein Family and Its Use for
; TITLE OF INVENTION: Immunomodulatory Purposes
; FILE REFERENCE: A041 US
; CURRENT APPLICATION NUMBER: US/10/696,259
; CURRENT FILING DATE: 2003-10-28
; PRIOR APPLICATION NUMBER: US/09/560,855A
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: PCT/US98/23826
; PRIOR FILING DATE: 1998-11-05
; PRIOR APPLICATION NUMBER: 60/064761
; PRIOR FILING DATE: 1997-11-07
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 671
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-696-259-1
```

Alignment Scores:

Pred. No.:	7,32e-90	Length:	671
Score:	848.00	Matches:	172
Percent Similarity:	89.7%	Conservative:	2
Best Local Similarity:	88.7%	Mismatches:	8
Query Match:	79.5%	Indels:	13
DB:	7	Gaps:	2

```
US-10-696-259-6 (1-201) x US-10-696-259-1 (1-671)
Qy 1 MetAlaTrpMetLeuLeuLeuLeuMetValHisProGlySerCysAlaLeuTrp 20
Db 66 ATGGCCCTGGATGCTGTTGCTCACTTATGATCATGTGTCCATCAGGATCTCTGTGCTCTCGG 125
Qy 21 ValSerGlnProGluLeuLeuArgThrLeuGluGlySerSerAlaPheLeuProCysSer 40
Db 126 GTGTCCAGCCCCCTGAGATTCTGTACCTCGAAGGATCTCTGCTTCTCTGCTGCTGCTCC 185
Qy 41 PheAsnAlaSerGlnGlyArgLeuAlaLeuGlySerValThrTrpPheArgAspGluVal 60
Db 186 TTCAATCCCAAGCAAGGAGACTGGCCATTTGGCTCCGTCAGCTGGTTCGAGATGAGGTG 245
Qy 61 ValProGlyLysGluValArgAsnGlyThrProGluPheArgGlyArgLeuAlaProLeu 80
Db 246 GTTCCAGGAGGAGGTGAGGATGGAACTCCAGAGTTTCCAG-GGGCCCTGGCCCCACTT 304
Qy 81 AlaSerSerArgPheLeuHisAspHisGlnAlaGluLeuHisLeuArgAspValArgGly 100
Db 305 GCTTCTTCCCGTTTCTTCCATGACCACAGGCTGAGCTGCACATCCGGGAGCTCGGAGGC 364
Qy 101 HisAspAlaSerIleTyrValCysArgValGluValLeuGlyLeuGlyValGlyThrGly 120
Db 365 CATGACCCAGCATCTACGTGTGCAGAGTGGAGGTGCTGGGCTTGTGTGGGACAGGG 424
Qy 121 AsnGlyThrArgLeuValValGluLysGluHisProGlnLeuGlyAlaGlyThrValLeu 140
Db 425 AATGGGACTCGGCTGGTGGTGGAGAAAGAAACATCTCAGCTAGGGGCTGGTACAGTCTCT 484
Qy 141 LeuLeuArgAlaGlyPheTyrAlaValSerPheLeuSerValAlaValGlySerThrVal 160
Db 485 CTCTTCGGGCTGGATTCTATGCTGTGTCAGCTTCTCTCTGTGGCCGTGGGAGCAGCCGTC 544
Qy 161 TyrTyrGlnGlyLys-----CysLeuThrTrpLysGlyPro 172
Db 545 TATTACCAGGGCAAAATGCCACTGTACATGGGAACACACTGCCACTCTCAGATGGGCCC 604
Qy 173 ArgArgGlnLeuProAlaValValProAlaProLeuProPro 186
Db 605 CGA-----GGAGTGATTCCAGAGCCAGATGTCCC 634
RESULT 12
US-08-973-544-1/c
; Sequence 1, Application US/08973544
; Publication No. US20010010926A1
; GENERAL INFORMATION:
; APPLICANT: WEISS, Elisabeth
; TITLE OF INVENTION: NEW IMMUNOREGULATORY PROTEIN LST-1
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIKAIIDO, MARCELSTEIN, MURRAY & ORAM LLP
; STREET: 655 Fifteenth St., NW, Suite 300, G St. Lobby
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-5701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/973,544
; FILING DATE: 18-DEC-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT EP 96/02663
; FILING DATE: 20-JUN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95109511.6
; FILING DATE: 20-JUN-1995
```

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95112201.9
; FILING DATE: 03-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Kitta, Monica Chin
; REGISTRATION NUMBER: 36,105
; REFERENCE/DOCKET NUMBER: P8341-7073
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 638-5000
; TELEFAX: (202) 638-4810
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5581 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: exon
; LOCATION: 48..162
; FEATURE:
; NAME/KEY: exon
; LOCATION: 544..652
; FEATURE:
; NAME/KEY: exon
; LOCATION: 1044..1162
; FEATURE:
; NAME/KEY: exon
; LOCATION: 1475..1567
; FEATURE:
; NAME/KEY: exon
; LOCATION: 1775..1797
; FEATURE:
; NAME/KEY: exon
; LOCATION: 2325..2709
US-08-973-544-1

Alignment Scores:
Pred. No.: 7,29e-80 Length: 5581
Score: 773.00 Matches: 181
Percent Similarity: 51.1% Conservative: 0
Best Local Similarity: 51.1% Mismatches: 4
Query Match: 72.4% Indels: 171
DB: 2 Gaps: 3

US-10-696-259-6 (1-201) x US-08-973-544-1 (1-5581)

Qy 16 SerCysAlaLeuTrpValSerGlnProGluLeuArgThrLeuGluGlySerSerala 35
Db 3948 TCCTGTCTCTGGGTGTCAGCCCTGAGATTGCTACCTGGAAGGATCCTCTGCC 3889
Qy 36 PheLeuProCysSerPheAsnAlaSerGlnGlyArgLeuAlaIleGlySerValThrTrp 55
Db 3888 TTCTGCCCTCTCTCTCAATGCCAGCAAGGAGACTGGCCATTGGCTCCGTCCACGTGG 3829
Qy 56 PheArgAspGluValValProGlyLysGluValArgAsnGlyThrProGluPheArgGly 75
Db 3828 TTCCAGATGAGTGGTTCCAGGGAGAGAGTGGAGATGAACCCAGATTTCAGGGGC 3769
Qy 76 ArgLeuAlaProLeuAlaSerSerArgPheLeuHisAspHisGlnAlaGluLeuHisIle 95
Db 3768 GGCCT---CCATCTGCTTCTCCGTTTCTCCATGACACCAGGCTGAGCTGCACATC 3713
Qy 96 ArgAspValArgGlyHisAspAla-SerIleTrpValCysArgValGluValLeuGlyLe 115
Db 3712 CGGACGTGCGAGGCCATGACGCCAGGCACTACGTGTGCAGAGTGGAGGTGCTGGGCCT 3653
Qy 115 uGlyValGlyThrGlyAsnGlyThrArgLeuValValGluLys----- 129
Db 3652 TGGTGTGGGACAGGGAATGGGATCTCGGCTGGTGGAGAAAGGTGAGATGCTGGGAGG 3593
Qy 129 ----- 421

Db 3592 TGGTGTCTCTCTGGGTGAGGCCCAAGAGCAATGTCTCTGGGAGGAGGATGCTCC 3533
Qy 129 ----- 129
Db 3532 TCTGAGGCCCTTCCCTCCCTGAGCCTGTGTGCATCTTCTTCCCAACCCCGTCTCOATT 3473
Qy 130 -----GluHisProGlnLeu-GlyAlaGlyThrValLeuLeuLeuArgAlaGlyP 146
Db 3472 GCCCATGCGAGACATCTCTAGTAGGGGCTGGTACAGTCTCTCT-CTTCGGGCTGGAT 3414
Qy 146 heTyralaValSerPheLeuSerValAlaValGlySerThrValTyTyrGlnGlyLysC 166
Db 3413 TCTATGTGTGAGCTTCTCTGTGGCCGTGGGACGACCGTCTATTACAGGGCAAT 3354
Qy 166 ys----- 166
Db 3353 GTGAGTAATGGAGCCAGGGGCAATAGTGGACGGATGGGAGGGGACGTAAGAGAGTGGGA 3294
Qy 166 ----- 166
Db 3293 GGAGGAGGACAGAGACCAGGAGAGAGAGCCCTCGGACTGCACTGAGCAGCTCCT 3234
Qy 166 ----- 166
Db 3233 GTCTCTCTCTGACGAGGCCACTGTGCATGGAACACACTGCCACTCTCTCAGATGGCC 3174
Qy 166 ----- 166
Db 3173 CCGAGGAGTGATTCAGAGCCAGATGTCCCTAGTCTCTTCAAAAGAGCCCAATAATC 3114
Qy 166 ----- 166
Db 3113 TGCCCCACCACTAACTCTCATGAGTCTCAAGTGTCTTCTTCCATTCTCCAGATGCCA 3054
Qy 167 -----LeuThrTrp 169
Db 3053 AATCTACTCTCTCGGATTCGCCCACTCTGAACTTTCCTTCCACCAGGTCTGACCTGG 2994
Qy 170 LysGlyProArgGlnLeuProAlaValValProAlaProLeuProProCysGly 189
Db 2993 AAAGGTCCAAGAAGGAGCTGCCGGCTGTGGTCCAGCGCCCTCCACCACCATGTGGG 2934
Qy 190 SerSerAlaHisLeuLeuProValProValProGlyGly 201
Db 2933 AGCTCAGCACATCTGCTTCCCGCCAGTCCCGAGGAGGC 2898
RESULT 13
US-10-036-444-10
; Sequence 10, Application US/10036444
; Publication No. US20020142445A1
; GENERAL INFORMATION:
; APPLICANT: INNATE PHARMA S.A.S.
; APPLICANT: UNIVERSITA DI GENOVA
; TITLE OF INVENTION: "No. US20020142445A1e1 triggering receptor involved in natural
; TITLE OF INVENTION: cytotoxicity mediated by human Natural Killer cells and
; FILE REFERENCE: SEQ-PR-1060
; CURRENT APPLICATION NUMBER: US/10/036,444
; PRIOR FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: 09/440,514
; PRIOR FILING DATE: 1999-11-15
; PRIOR APPLICATION NUMBER: 09/456,199
; PRIOR FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 421
; TYPE: DNA
; ORGANISM: Human NK cell
US-10-036-444-10
Alignment Scores: 5.64e-76 Length: 421
Pred. No.: 421

Db 181 GTTCCAGGGAAGGAGGTGAGGAATGGAACCCAGAGTTTCAGGGGCCGCTGGCCCACTT 240
QY 81 AlaSerSerArgPheLeuHisAspHisGlnAlaGluLeuHisIleArgAspValArgGly 100
Db 241 GCTTCTTCCCGTTTCTCCATGACCAACCCAGGCTGAGCTGCACATCCGGGACGTGCGAGGC 300
QY 101 HisAspAlaSerIleTyrValCysArgValGluValLeuGlyLeuGlyValGlyThrGly 120
Db 301 CATGACGCCAGCATCTACGTGTGCAGAGTGGAGGTGCTGGGCCTTGGTGTCTGGGACAGGG 360
QY 121 AsnGlyThrArgLeuValValGluLysGluHisProGlnLeuGly 135
Db 361 AATGGGACTCGGCTGGTGGTGGAGAAAGACATCCTCAGCTAGGG 405

Search completed: February 28, 2006, 07:27:06
Job time : 786 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: February 28, 2006, 07:06:37 ; Search time 322 Seconds
(without alignments)
1331.074 Million cell updates/sec

Title: US-10-696-259-6

Perfect score: 1067
Sequence: 1 MAMWLLILIMVHGSCALW.....APLPPCGSAHLLPPVPG 201

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 7209121 seqs, 1066183437 residues

Total number of hits satisfying chosen parameters: 14418242

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n model -DEV=xlh
-Q=/abs/ASSWEB_spool/US10696259/runat_27022006_123603_27334/app_query.fasta_1
-DB=Published Applications NA New -QFMT=fastap -SUFFIX=p2n.rnpbn -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bites -START=1 -END=1 -MATRIX=bl0sum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pt0 -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -HOST=abs04
-USER=US10696259 -CGN 1_1220 -runat 27022006_123603_27334 -NCPUS=6 -ICPU=3
-NO MMAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA New:

- 1: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq.*
- 2: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq.*
- 3: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq.*
- 4: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq.*
- 5: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq.*
- 6: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq.*
- 7: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq.*
- 8: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq.*
- 9: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq.*
- 10: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq.*
- 11: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq.*
- 12: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq.*
- 13: /cgn2_6/ptodata/2/pubpna/US160_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	855	80.1	40000	8	US-10-995-561-13510 Sequence 13510, A
C 2	853.5	80.0	6853	12	US-11-122-329-89 Sequence 89, Appl
C 3	347	32.5	201	8	US-10-995-561-84078 Sequence 84078, A
C 4	308	28.9	201	8	US-10-995-561-84065 Sequence 84065, A

c	5	199	18.7	201	8	US-10-995-561-84088	Sequence 84088, A
c	6	195	18.3	201	8	US-10-995-561-83983	Sequence 83983, A
c	7	194	18.2	201	8	US-10-995-561-84144	Sequence 84144, A
c	8	193	18.1	201	8	US-10-995-561-84089	Sequence 84089, A
c	9	187	17.5	201	8	US-10-995-561-84082	Sequence 84082, A
c	10	154.5	14.5	201	8	US-10-995-561-84087	Sequence 84087, A
	11	122	11.4	2754	8	US-10-821-234-163	Sequence 163, Appl
	12	120	11.2	1107	12	US-11-000-688-10	Sequence 10, Appl
	13	115	10.8	724	12	US-11-136-527-3003	Sequence 3003, Ap
	14	113.5	10.6	2220	9	US-11-072-512-1739	Sequence 1739, Ap
	15	110.5	10.4	2467	12	US-11-080-991-107	Sequence 107, App
	16	110.5	10.4	2479	8	US-10-955-054A-50	Sequence 50, Appl
	17	106	9.9	2980	7	US-10-511-538-228	Sequence 228, App
	18	98	9.2	1650	12	US-11-000-463-12	Sequence 12, Appl
	19	98	9.2	1650	12	US-11-072-512-1263	Sequence 1263, Ap
	20	98	9.2	2036	12	US-11-136-527-2698	Sequence 2698, Ap
	21	97.5	9.1	822	8	US-10-623-155-440	Sequence 440, App
	22	97	9.1	930	12	US-11-000-463-107	Sequence 107, App
	23	97	9.1	5130	8	US-10-453-372-409	Sequence 409, App
	24	97	9.1	5130	12	US-11-135-855-12	Sequence 12, Appl
	25	97	9.1	5158	12	US-11-135-855-13	Sequence 13, Appl
	26	96.5	9.0	705	12	US-11-139-499-1	Sequence 1, Appli
c	27	95	8.9	894	12	US-11-000-463-484	Sequence 484, App
	28	94.5	8.9	1825	12	US-11-000-463-579	Sequence 579, App
	29	94	8.8	531	6	US-09-925-065A-423935	Sequence 423935,
	30	94	8.8	600	12	US-11-136-527-7099	Sequence 7099, Ap
	31	94	8.8	870	8	US-10-276-233A-4	Sequence 4, Appli
	32	94	8.8	933	8	US-10-623-155-439	Sequence 439, App
	33	93.5	8.8	4406	9	US-11-072-512-979	Sequence 979, App
	34	93.5	8.8	4947	8	US-10-995-561-457	Sequence 457, App
	35	93.5	8.8	6719	8	US-10-995-561-456	Sequence 456, App
	36	93	8.7	1019	8	US-10-775-169-232	Sequence 232, App
c	37	92.5	8.7	998	8	US-10-750-185-45237	Sequence 45237, A
c	38	92.5	8.7	998	8	US-10-750-623-45237	Sequence 45237, A
	39	92.5	8.7	5103	8	US-10-453-372-397	Sequence 397, App
	40	92.5	8.7	5103	8	US-10-453-372-411	Sequence 411, App
	41	92.5	8.7	5103	8	US-10-453-372-413	Sequence 413, App
	42	92.5	8.7	5103	8	US-10-453-372-415	Sequence 415, App
	43	92.5	8.7	5103	8	US-10-453-372-417	Sequence 417, App
	44	92	8.6	648	8	US-10-374-954-6	Sequence 6, Appli
	45	92	8.6	971	5	US-09-978-360A-214	Sequence 214, App

ALIGNMENTS

RESULT 1

US-10-995-561-13510/c
; Sequence 13510, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13510
; LENGTH: 40000
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(40000)
; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1
US-10-995-561-13510

Alignment Scores:
Pred. No.: 7.97e-63
Score: 855.00
Percent Similarity: 51.6%
Length: 40000
Matches: 188
Conservative: 1


```
Db 4800 TCTGAGGCCCTTCCCTCCCTGAGCGTGTGTGACATCTTCTCCCAACCCCGCTCTCCATT 4741
Qy 130 -----GluHisProGlnLeuGlyAlaGlyThrValLeuLeuLeuArgAlaGlyPh 146
Db 4740 GCCCATGCAACATCTCAGCTAGGGCTGGTACAGTCTCTCTCTCTGGGCTGGATT 4681
Qy 146 eTyrAlaValSerPheLeuSerValAlaValGlySerThrValTyrThrGlnGlyLysCy 166
Db 4680 CTATGCTGTAGCTTCTCTCTGTGGCGGTGGGAGCAGCACCGTCTATTACCGAGGCAATG 4621
Qy 166 s----- 166
Db 4620 TGAGTAATGGAGCCAGGGGCAATAGTGGACGGGATGGAGGGGCGAGTAAGAGAGTGGAG 4561
Qy 166 ----- 166
Db 4560 GAGGAGGACAGACAGACAGAGAGAGAGAGCGCTCGGGACTGCAACACTGACAGCTCTG 4501
Qy 166 ----- 166
Db 4500 TCCTCTCTGACGAGGCCACTGTACATGGGAACACACTGCCACTCTCTCAGATGGGCC 4441
Qy 166 ----- 166
Db 4440 CGAGGAGTATCCAGAGCCAGATGTCCTAGTCCCTTCTTCAAAAGACCCCAATAATCT 4381
Qy 166 ----- 166
Db 4380 GCCCACCACCTAATCTCTCATGAGTCTCAAGTGTTCCTTCTCCATCTCCAGATGCCAA 4321
Qy 167 -----LeuThrTrpL 170
Db 4320 ATCTACTCTCTCGGATTCCTCCCAACTCTGAACTTTCCTTCCACAGGTCTGACCTGGA 4261
Qy 170 yGlyProArgGlnLeuProAlaValValProAlaProLeuProProProCysGlyS 190
Db 4260 AAGTCCAAAGAGCAGTCCGCGTGTGTGCCAGCGCCCTCCACCACTGTTGGGA 4201
Qy 190 erSerAlaHisLeuLeuProProValProGlyGly 201
Db 4200 GCTCAGCACATCTCTTCCCTCCCTCCAGTCCAGGAGGC 4166

RESULT 3
US-10-995-561-84078/c
; Sequence 84078, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 84078
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-84078
Alignment Scores:
Pred. No.: 2,36e-21 Length: 201
Score: 347.00 Matches: 66
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 32.5% Indels: 0
DB: 8 Gaps: 0

US-10-696-259-6 (1-201) x US-10-995-561-84078 (1-201)
Qy 20 TrpValSerGlnProGluIleArgThrLeuGlySerSerAlaPheLeuProCys 39
```

```
Db 199 TGGGTGCCAGCCCTGAGATTCGTACCTCGAAGGATCCTCTGCTTCTCTGCGCTGC 140
Qy 40 SerPheAsnAlaSerGlnGlyArgLeuAlaIleGlySerValThrTrpPheArgAspGlu 59
Db 139 TCCTTCATGCCAGCCAGGAGACTGGCCATTGGCTCTGTCAGTGTGTTCCGAGATGAG 80
Qy 60 ValValProGlyLysGluValArgAsnGlyThrProGluPheArgGlyArgLeuAlaPro 79
Db 79 GTGGTTCAGGGAAGGAGGTGAGGAATGGAACCCAGAGTTTCAGGGGCGCGCTGGCCCA 20
Qy 80 LeuAlaSerSerArgPhe 85
Db 19 CTGCTTCTTCCCGTTTC 2

RESULT 4
US-10-995-561-84065/c
; Sequence 84065, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 84065
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-84065
Alignment Scores:
Pred. No.: 5.41e-18 Length: 201
Score: 308.00 Matches: 59
Percent Similarity: 98.3% Conservative: 0
Best Local Similarity: 98.3% Mismatches: 1
Query Match: 28.9% Indels: 0
DB: 8 Gaps: 0

US-10-696-259-6 (1-201) x US-10-995-561-84065 (1-201)
Qy 70 ThrProGluPheArgGlyArgLeuAlaProLeuAlaSerSerArgPheLeuHisAspHis 89
Db 200 ACCCCAGAGTTCAGGGCGCCCTGGCCCACTTGTCTTCTCCGTTTCTCCATGACCAC 141
Qy 90 GlnAlaGluLeuHisIleArgAspValArgGlyHisAspAlaSerIleTyrValCysArg 109
Db 140 CAGGCTGAGTGCACATCCGGAGCGTGGAGGCCATGACRCCAGCATCTACGTGTGCAGA 81
Qy 110 ValGluValLeuGlyLeuGlyValGlyThrGlyAsnGlyThrArgLeuValGluLys 129
Db 80 GTGAGGTGCTGGGCTTGTGTGTCGGACAGGGAATGGGACTCGGCTGTGTGGAGAAA 21

RESULT 5
US-10-995-561-84088/c
; Sequence 84088, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 84088
; LENGTH: 201
```

```

; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-84088

Alignment Scores:
Pred. No.: 1.33e-08 Length: 201
Score: 199.00 Matches: 35
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 18.7% Indels: 0
DB: 8 Gaps: 0

US-10-696-259-6 (1-201) x US-10-995-561-84088 (1-201)
QY 167 LeuThrTrpLysGlyProArgGlnLeuProAlaValProAlaProLeuProPro 186
Db 130 CTGACCTGGAAAGGTCGAAGAGGAGCTCCGGCTGTGGTCCAGCGCCCTCCACCA 71
QY 187 ProCysGlySerSerAlaHisLeuLeuProProValProGlyGly 201
Db 70 CCATGTGGAGCTCAGCACATCTGCTTCCCCAGTCCAGGAGGC 26

RESULT 6
US-10-995-561-83983/c
; Sequence 83983, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 83983
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-83983

Alignment Scores:
Pred. No.: 2.94e-08 Length: 201
Score: 195.00 Matches: 34
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 18.3% Indels: 0
DB: 8 Gaps: 0

US-10-696-259-6 (1-201) x US-10-995-561-83983 (1-201)
QY 168 ThrTrpLysGlyProArgGlnLeuProAlaValProAlaProLeuProProPro 187
Db 199 ACCTGGAAAGGTCGAAGAGGAGCTCCGGCTGTGGTCCAGCGCCCTCCACCA 140
QY 188 CysGlySerSerAlaHisLeuLeuProProValProGlyGly 201
Db 139 TGTGGAGCTCAGCACATCTGCTTCCCCAGTCCAGGAGGC 98

RESULT 7
US-10-995-561-84144/c
; Sequence 84144, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 84144
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-84144

Alignment Scores:
Pred. No.: 3.59e-08 Length: 201
Score: 194.00 Matches: 38
Percent Similarity: 95.0% Conservative: 0
Best Local Similarity: 95.0% Mismatches: 2
Query Match: 18.2% Indels: 0
DB: 8 Gaps: 0

US-10-696-259-6 (1-201) x US-10-995-561-84144 (1-201)
QY 130 GluHisProGlnLeuGlyAlaGlyThrValLeuLeuArgAlaGlyPheTyrAlaVal 149
Db 136 GAACATCCTCAGCTAGGGCTGGTACAGTCTCTWCTTGGGCTGGATTCTATGCTGTC 77
QY 150 SerPheLeuSerValAlaValGlySerThrValTyrTyrGlnGlyLysCysLeuThrTrp 169
Db 76 AGCTTCTCTCTGTGGCCGTGGCAGCAGCGTCTATTACAGGCAAAATGTGAGTAATGG 17

RESULT 8
US-10-995-561-84089/c
; Sequence 84089, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 84089
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-84089

Alignment Scores:
Pred. No.: 4.38e-08 Length: 201
Score: 193.00 Matches: 34
Percent Similarity: 97.1% Conservative: 0
Best Local Similarity: 97.1% Mismatches: 1
Query Match: 18.1% Indels: 0
DB: 8 Gaps: 0

US-10-696-259-6 (1-201) x US-10-995-561-84089 (1-201)
QY 167 LeuThrTrpLysGlyProArgGlnLeuProAlaValProAlaProLeuProPro 186
Db 124 CTGACCTGGAAAGGTCGAAGAGGAGCTCCGGCTGTGGTCCAGCGCCCTCCACCA 65
QY 187 ProCysGlySerSerAlaHisLeuLeuProProValProGlyGly 201
Db 64 CCATGTGGAGCTCAGCACATCTGCTTCCCCAGTCCAGGAGGC 20

RESULT 9
US-10-995-561-84082/c
; Sequence 84082, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 84082
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-84082
```


**This Page is Inserted by IFW Indexing and Scanning
Operations and is not part of the Official Record**

BEST AVAILABLE IMAGES

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images include but are not limited to the items checked:

☐ BLACK BORDERS

☒ IMAGE CUT OFF AT TOP, BOTTOM OR SIDES

☐ FADED TEXT OR DRAWING

☐ BLURRED OR ILLEGIBLE TEXT OR DRAWING

☐ SKEWED/SLANTED IMAGES

☐ COLOR OR BLACK AND WHITE PHOTOGRAPHS

☐ GRAY SCALE DOCUMENTS

☐ LINES OR MARKS ON ORIGINAL DOCUMENT

☒ REFERENCE(S) OR EXHIBIT(S) SUBMITTED ARE POOR QUALITY

☐ OTHER: _____

IMAGES ARE BEST AVAILABLE COPY.

As rescanning these documents will not correct the image problems checked, please do not report these problems to the IFW Image Problem Mailbox.

THIS PAGE BLANK (USPTO)